GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 23:33:52 ; Search time 406 Seconds
(without alignments)
3038.458 Million cell updates/sec

Title: US-09-914-053A-5
Perfect score: 1241
Sequence: 1 MSIWTSGRTSSSYRHDEKRN.....MVKLTQYLSLLCERIQRINR 235

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09914053/runat_04112004_183921_18210/app_query.fasta_1.391
-DB=N_Geneseq_23Sep04 -QFMT=fastap -SUFFIX=rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15
-MODE=LOCAL -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09914053_@CGN_1_1_708_@runat_04112004_183921_18210 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1235	99.5	1184	4	AAF27991	Aaf27991 Human cal
2	1228	99.0	1300	3	AAZ51632	Aaz51632 Human mem
3	1216	98.0	707	3	AAA75011	Aaa75011 DNA encod
4	1012	81.5	2098	3	AAA26355	Aaa26355 Human sec
5	1012	81.5	2098	8	ADA39669	Ada39669 Human sec
6	1012	81.5	2098	10	ADA55858	Ada55858 Gene enco
7	1012	81.5	2098	12	ADL71416	Adl71416 Novel hum
8	481.5	38.8	1246	2	AAZ11912	Aaz11912 Human pot
9	481	38.8	558	4	ABA09433	Aba09433 Human K c
10	478.5	38.6	1237	4	AAF27992	Aaf27992 Human cal
11	478	38.5	1111	2	AAZ11913	Aaz11913 Human pot
12	477.5	38.5	1144	4	AAK52128	Aak52128 Human pol
13	477.5	38.5	1251	4	ABA09214	Aba09214 Human Ca-
14	477.5	38.5	1251	4	AAK53112	Aak53112 Human pol
15	474	38.2	774	3	AAA75009	Aaa75009 DNA encod
16	474	38.2	1296	4	AAF27995	Aaf27995 Human cal
17	474	38.2	1632	4	AAF27993	Aaf27993 Human cal
18	464.5	37.4	1759	4	AAF27994	Aaf27994 Human cal
19	421	33.9	1106	2	AAT06477	Aat06477 Human cal
20	421	33.9	1277	6	ABL69681	Abl69681 Prostate
21	421	33.9	1277	10	ADD14749	Add14749 Human src
22	383	30.9	2238	2	AAT06476	Aat06476 Bovine ca
23	352	28.4	608	4	AAL02267	Aal02267 Human rep
24	319	25.7	1228	2	AAX82099	Aax82099 Human cal
25	318	25.6	1501	3	AAC75815	Aac75815 Human ORF
26	318	25.6	1608	3	AAZ22298	Aaz22298 Human pot
27	316	25.5	633	3	AAA75010	Aaa75010 DNA encod
c 28	207	16.7	110000	12	ADO34927_0	Ado34927 Human vol
c 29	195	15.7	7045	4	ABA07292	Aba07292 Human pan
c 30	195	15.7	7045	4	AAK89937	Aak89937 Human dig
31	195	15.7	7045	4	AAL37429	Aal37429 Human mus
32	195	15.7	7045	8	ABX60417	Abx60417 cDNA enco
33	195	15.7	7045	12	ADJ31167	Adj31167 Human mus
34	177	14.3	394	3	AAC03613	Aac03613 Human sec
35	151.5	12.2	898	6	ABQ25377	Abq25377 Oligonucl
c 36	151.5	12.2	898	6	ABQ25376	Abq25376 Oligonucl
37	150	12.1	285	2	AAT22677	Aat22677 Human gen
38	148	11.9	898	6	ABQ25374	Abq25374 Oligonucl
c 39	148	11.9	898	6	ABQ25375	Abq25375 Oligonucl
40	138.5	11.2	48000	4	AAF27996	Aaf27996 Human cal
41	132	10.6	188	3	AAC07442	Aac07442 Human sec
42	125.5	10.1	2787	5	AAS77593	Aas77593 DNA encod
43	125.5	10.1	2787	5	AAS82312	Aas82312 DNA encod
44	125.5	10.1	2787	5	AAS77413	Aas77413 DNA encod
c 45	120.5	9.7	345	12	ADO35048	Ado35048 Human KCh

ALIGNMENTS

RESULT 1
AAF27991
ID AAF27991 standard; DNA; 1184 BP.
XX
AC AAF27991;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human calcium sensitive potassium channel beta2 subunit coding sequence.
XX
KW Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW irritable bowel syndrome; Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
PN WO200105828-A1.
XX
PD 25-JAN-2001.
XX
PF 18-JUL-2000; 2000WO-US019585.
XX
PR 20-JUL-1999; 99US-0144764P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Uebele V, Swanson R, Liu Y, Lagrutta A;
XX
DR WPI; 2001-159514/16.

```
DR   P-PSDB; AAB35301.
XX
PT   Novel human calcium sensitive potassium channel subunits for identifying
PT   inhibitors and agonists of the potassium channel for use in treating
PT   conditions such as asthma, hypertension, memory disorders, depression.
XX
PS   Claim 3; Fig 1A; 89pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC   and beta3d subunits. These can be used to identify inhibitors and
CC   activators of the channels, which can be used in the treatment of
CC   conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC   Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC   incontinence, migraine and irritable bowel syndrome. The coding sequences
CC   are found at human chromosome 3q23-ter. The present sequence is the beta2
CC   subunit coding sequence
XX
SQ   Sequence 1184 BP; 356 A; 260 C; 255 G; 313 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              5.92e-134       Length:         1184
Score:                  1235.00         Matches:        234
Percent Similarity:     99.57%          Conservative:   0
Best Local Similarity:  99.57%          Mismatches:     1
Query Match:            99.52%          Indels:         0
DB:                     4               Gaps:           0

US-09-914-053A-5 (1-235) x AAF27991 (1-1184)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 330

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 390

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 450

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 510

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 570

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 630

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 690

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 750

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 810

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        811 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 870

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 930

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db        931 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 975

RESULT 2
AAZ51632
ID   AAZ51632 standard; cDNA; 1300 BP.
XX
AC   AAZ51632;
XX
DT   21-JUN-2000  (first entry)
XX
DE   Human membrane channel protein-16 (MECHP-16) cDNA.
XX
KW   Membrane channel protein-16; MECHP-16; diagnosis; treatment; lymphoma;
KW   cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;
KW   inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
KW   diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
KW   muscular disorder; myocarditis; Duchenne's muscular dystrophy; nootropic;
KW   cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiant;
KW   neurological disorder; Alzheimer's disease; Parkinson's disease; human;
KW   Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;
KW   anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
KW   hypotensive; vasotropic; antiasthmatic; antiinflammatory; antidepressant;
KW   anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             378. .1085
FT                   /*tag=  a
FT                   /product= "MECHP-16"
FT                   /note= "Shows homology to human beta subunit of Ca+
FT                   activated K+ channel"
FT   misc_binding    381. .425
FT                   /*tag=  b
FT                   /bound_moiety= "Primer or Probe"
XX
PN   WO200012711-A2.
XX
PD   09-MAR-2000.
XX
PF   02-SEP-1999;   99WO-US020468.
XX
PR   02-SEP-1998;   98US-0155226P.
PR   12-NOV-1998;   98US-00191283.
PR   09-DEC-1998;   98US-0155225P.
PR   26-JAN-1999;   99US-0155211P.
PR   10-FEB-1999;   99US-0155263P.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Bandman O,  Tang YT,  Reddy R,  Hillman JL,  Yue H;
PI   Lal P,  Corley NC,  Guegler KJ,  Gorgone G,  Baughn MR,  Azimzai Y;
XX
DR   WPI; 2000-256643/22.
DR   P-PSDB; AAY70466.
XX
PT   Novel human membrane channel protein and polynucleotide useful for
PT   diagnosing and treating cell proliferative, inflammatory, secretory,
PT   osmoregulatory, muscular, cardiovascular and neurological disorders.
XX
PS   Claim 9; Page 128-129; 140pp; English.
XX
CC   The present sequence is a cDNA identified in Incyte clone 2069907 derived
CC   from ISLTNOT01 cDNA library. It encodes human membrane channel protein-16
CC   (MECHP-16), which is expressed in nervous tissues. Anti-MECHP antibodies
CC   can be used as therapeutic antagonists and reagents for diagnosis and
CC   monitoring diseases. MECHP cDNA can be used for diagnosis of MECHP-
CC   related diseases and gene mapping. MECHP can be used for treatment of
CC   cell proliferative disorders such as bursitis and atherosclerosis,
CC   cancers like lymphoma and sarcoma, inflammatory disorders like AIDS and
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CC   Addison's disease, transport/secretory disorders like cystic fibrosis and
CC   diabetes mellitus, osmoregulatory disorders like diarrhoea and renal
CC   failure, muscular disorders like myocarditis and Duchenne's muscular
CC   dystrophy, cardiovascular disorders like hypertension and vasculitis,
CC   congenital lung anomalies like bronchitis and asthma and neurological
CC   disorders like Alzheimer's disease, Parkinson's disease and Huntington's
CC   disease
XX
SQ   Sequence 1300 BP; 381 A; 288 C; 279 G; 352 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              4.48e-133       Length:         1300
Score:                  1228.00         Matches:        233
Percent Similarity:     99.15%          Conservative:   0
Best Local Similarity:  99.15%          Mismatches:     2
Query Match:            98.95%          Indels:         0
DB:                     3               Gaps:           0

US-09-914-053A-5 (1-235) x AAZ51632 (1-1300)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 437

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 497

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 557

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 617

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 677

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||  ||||||||||||||||||||||||
Db        678 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCCCCAGGTGTACGTTAACCTG 737

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 797

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 857

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 917

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        918 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 977

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 1037

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1038 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 1082

RESULT 3
AAA75011
ID   AAA75011 standard; DNA; 707 BP.
XX
AC   AAA75011;
XX
DT   02-JAN-2001  (first entry)
XX
DE   DNA encoding a human BK beta-4 polypeptide.
XX
KW   Human; BK beta-2; beta subunit; Slo potassium channel; BK beta-3;
KW   BK beta-4; ion flux; migraine; hearing; vision problem; seizure; stroke;
KW   asthma; cell proliferation; hormone secretion; cancer; viral infection;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .707
FT                   /*tag=  a
FT                   /product= "BK beta-4"
FT                   /transl_except= (pos: 691. .692, aa: Gln)
XX
PN   WO200050444-A1.
XX
PD   31-AUG-2000.
XX
PF   22-FEB-2000; 2000WO-US004441.
XX
PR   23-FEB-1999;   99US-0121224P.
PR   03-NOV-1999;   99US-0163367P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ,  Wickenden A,  Liu Y;
XX
DR   WPI; 2000-533179/48.
DR   P-PSDB; AAB08820.
XX
PT   Isolated beta subunit polynucleotides and polypeptides of Slo potassium
PT   channels are used to determine the effects of compounds on ion flux
PT   through a potassium channel and in computer modelling systems.
XX
PS   Claim 7; Page 79-80; 84pp; English.
XX
CC   The present sequence encodes a human BK beta-4 polypeptide. The
CC   polypeptide is a beta subunit of a Slo potassium channel. The
CC   specification also describes BK beta-3 and BK beta-3 polypeptides. BK
CC   beta subunits are auxiliary subunits or monomers of Slo potassium
CC   channels. The polypeptides, when expressed in cells and cell membranes,
CC   are used to determine the effects of compounds on ion flux through a
CC   potassium channel. The compounds identified may be useful as therapeutic
CC   agents e.g. modulators that target specific Slo channels are useful for
CC   treating migraines, hearing and vision problems, seizures, stroke,
CC   asthma, cell proliferation and hormone secretion. The computer generated
CC   3-dimensional structures of BK beta 2, BK beta 3 or BK beta 4 are used to
CC   identify ligands that bind to the beta subunit. The characterized BK beta
CC   subunits are used to determine how Slo potassium channels function in
CC   different environments and how they respond to different activation
CC   mechanisms. The polynucleotides are used to transfect cells in vivo and
CC   in vitro to mitigate effects of absent, partial inactivation or abnormal
CC   expression of the BK beta subunit gene e.g. to correct genetic defects,
CC   cancer and viral infection
XX
SQ   Sequence 707 BP; 205 A; 170 C; 153 G; 177 T; 0 U; 2 Other;

Alignment Scores:
Pred. No.:              4.53e-132       Length:         707
Score:                  1216.00         Matches:        234
Percent Similarity:     99.57%          Conservative:   0
Best Local Similarity:  99.57%          Mismatches:     1
Query Match:            97.99%          Indels:         1
DB:                     3               Gaps:           0

US-09-914-053A-5 (1-235) x AAA75011 (1-707)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              ||||||||||||||||||||||||||||||  ||||||||||||
Db        661 CAGTACCTCTCCCTACTATGTGAGAGGATCCA-CGGATCAATAGA 704
```

RESULT 4
AAA26355
ID AAA26355 standard; cDNA; 2098 BP.
XX
AC AAA26355;
XX
DT 29-JUN-2000 (first entry)
XX
DE Human secreted protein gene 10 SEQ ID NO:20.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO200006698-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-US017130.
XX
PR 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX
DR WPI; 2000-195282/17.
DR P-PSDB; AAY91460.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 378-379; 634pp; English.
XX
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.6e-107	Length:	2098
Score:	1012.00	Matches:	191
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	81.55%	Indels:	0
DB:	3	Gaps:	0

US-09-914-053A-5 (1-235) x AAA26355 (1-2098)

```
Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
```

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                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
                ||||||||||||||||||||||||||||||||
Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582
```

RESULT 5
ADA39669
ID ADA39669 standard; cDNA; 2098 BP.
XX
AC ADA39669;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;
KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 51; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.6e-107	Length:	2098
Score:	1012.00	Matches:	191
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	81.55%	Indels:	0
DB:	8	Gaps:	0

US-09-914-053A-5 (1-235) x ADA39669 (1-2098)

```
Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
                ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
                ||||||||||||||||||||||||||||||||
Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582
```

```
RESULT 6
ADA55858
ID   ADA55858 standard; DNA; 2098 BP.
XX
AC   ADA55858;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Gene encoding human secreted protein #37.
XX
KW   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW   cytostatic; cerebroprotective; neuroprotective; nootropic;
KW   cardiovascular; antiarteriosclerotic; gene therapy;
KW   human secreted protein; immune disorder; inflammation;
KW   respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW   inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW   multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW   Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW   triple helix formation; antisense gene therapy; forensic biology; ds;
KW   gene.
XX
OS   Homo sapiens.
XX
PN   WO2002102994-A2.
XX
PD   27-DEC-2002.
XX
PF   19-MAR-2002; 2002WO-US008278.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-167512/16.
DR   P-PSDB; ADA56755.
XX
PT   New human secreted polypeptides and polynucleotides, useful for
PT   diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT   conditions, respiratory disorders, cancers, CNS disorders, or
PT   neurodegenerative disorders.
XX
PS   Claim 21; SEQ ID NO 47; 1754pp; English.
XX
CC   The invention relates to 592 new human secreted polypeptides useful for
CC   diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC   conditions, respiratory disorders, cancers, CNS disorders, or
CC   neurodegenerative disorders, or polypeptides comprising an amino acid
CC   sequence at least 95% identical to the new sequences. The polypeptides,
CC   antibodies or antibody fragments that bind to the polypeptides, nucleic
CC   acids encoding the polypeptides, agonists or antagonists that binds to
CC   the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC   compositions for diagnosing, treating or preventing an e.g. immune
CC   disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC   nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC   allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC   (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC   disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC   cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC   polynucleotides are useful for chromosome identification, chromosome
CC   mapping, for controlling gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy, for identifying individuals
CC   from minute biological samples, in forensic biology, and as hybridization
CC   probes. The polypeptides are useful for as molecular weight markers on
CC   sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   gels, to raise antibodies, for testing biological activities, and for
CC   treating or preventing neural disorders, immune system disorders,
CC   muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC   renal, proliferative and/or cancerous diseases. This sequence corresponds
CC   to a gene encoding one of the polypeptide of the invention. Note: The
CC   sequence data for this patent did form part of the printed specification,
CC   but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.6e-107        Length:          2098
Score:                    1012.00         Matches:         191
Percent Similarity:       100.00%         Conservative:    0
Best Local Similarity:    100.00%         Mismatches:      0
Query Match:              81.55%          Indels:          0
DB:                       10              Gaps:            0

US-09-914-053A-5 (1-235) x ADA55858 (1-2098)

Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||
Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582

RESULT 7
ADL71416
ID   ADL71416 standard; cDNA; 2098 BP.
XX
AC   ADL71416;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Novel human secreted protein cDNA seqid 20.
XX
KW   antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; antilipaemic; CNS; gynaecological; antiarthritic;
KW   antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
KW   immunosuppressive; antiallergic; cardiovascular; respiratory;
KW   dermatological; antimicrobial; gastrointestinal; gene therapy;
KW   neurodegenerative disease; behavioral disorder; inflammatory condition;
KW   hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
```

```
KW   Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW   Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW   arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW   Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW   leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW   respiratory disorder; pulmonary disorder; connective tissue disorder;
KW   skin disorder; CNS disorder; congenital disorder; infectious disorder;
KW   gastrointestinal disorder; human; secreted protein; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2004034196-A1.
XX
PD   19-FEB-2004.
XX
PF   27-JAN-2003; 2003US-00351334.
XX
PR   30-JUL-1998;    98US-0094657P.
PR   05-AUG-1998;    98US-0095486P.
PR   06-AUG-1998;    98US-0095454P.
PR   06-AUG-1998;    98US-0095455P.
PR   12-AUG-1998;    98US-0096319P.
PR   29-JUL-1999;    99WO-US017130.
PR   24-JAN-2000; 2000US-00489847.
PR   25-JAN-2002; 2002US-0350898P.
XX
PA   (KOMA/) KOMATSOULIS G A.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (DUAN/) DUAN D R.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (WEIY/) WEI Y.
XX
PI   Komatsoulis GA,  Rosen CA,  Ruben SM,  Duan DR,  Moore PA,  Shi Y;
PI   Lafleur DW,  Wei Y;
XX
DR   WPI; 2004-180094/17.
DR   P-PSDB; ADL71532.
XX
PT   New human secreted nucleic acid, useful for diagnosing and treating
PT   neurodegenerative, inflammatory, hyperproliferative, metabolic,
PT   reproductive, cardiovascular, respiratory or immunological disorders or
PT   diseases.
XX
PS   Claim 1; SEQ ID NO 20; 234pp; English.
XX
CC   The invention describes an isolated human nucleic acid molecule (I)
CC   comprising a polynucleotide having a nucleotide sequence at least 95%
CC   identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
CC   the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
CC   to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
CC   epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
CC   sequence included in ATCC Deposit No: Z, which is hybridisable to SEQ ID
CC   NO: X, having a biological activity. The nucleic acids and polypeptides,
CC   pharmaceutical formulations and kits are useful in diagnosing and
CC   treating neurodegenerative diseases states, behavioral disorders,
CC   inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
CC   disease, Parkinson's diseases or Huntington's diseases), metabolic
CC   disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
CC   disorders, immunological disorders (e.g. arthritis, asthma or AIDS),
CC   endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
CC   or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
CC   cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
CC   conditions afflicting connective tissue, skin disorders, CNS disorders,
CC   congenital disorders, infectious disorders and gastrointestinal
CC   disorders. This sequence encodes a novel human secreted protein of the
CC   invention. Note: This sequence does not appear in the printed
CC   specification but is available in electronic format from the US patent
CC   office at ftp.seqdata.uspto.gov/seqdata.html?DocID=20040034196.
XX
SQ   Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;
```

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Alignment Scores:
Pred. No.:                1.6e-107      Length:          2098
Score:                    1012.00       Matches:         191
Percent Similarity:       100.00%       Conservative:    0
Best Local Similarity:    100.00%       Mismatches:      0
Query Match:              81.55%        Indels:          0
DB:                       12            Gaps:            0

US-09-914-053A-5 (1-235) x ADL71416 (1-2098)

Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||
Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582
```

```
RESULT 8
AAZ11912
ID   AAZ11912 standard; cDNA; 1246 BP.
XX
AC   AAZ11912;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov44 cDNA (splice variant 1).
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             432. .1094
FT                   /*tag=  a
FT                   /product= "Human K+Hnov44 potassium channel"
XX
PN   WO9943696-A1.
XX
```

```
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US003826.
XX
PR   25-FEB-1998;   98US-0076687P.
PR   07-AUG-1998;   98US-0095836P.
PR   19-JAN-1999;   99US-0116448P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Miller AP,  Curran ME,  Hu P,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; AAY34131.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
PT   useful for the diagnosis and treatment of episodic ataxia with myokymia,
PT   cardiac arrhythmia, epilepsy and Bartter's syndrome.
XX
PS   Claim 4; Page 89-90; 112pp; English.
XX
CC   This sequence represents splice variant 1 of a human potassium channel
CC   K+Hnov44 cDNA. Alternative splicing does not affect the amino acid
CC   sequence of the protein. K+Hnov proteins have a high degree of homology
CC   to known potassium channels and may be alpha subunits, which form the
CC   functional channel, or accessory subunits that act to modulate the
CC   channel activity. K+Hnov44 is a potassium channel beta subunit. The
CC   gene's chromosomal location is 22p13, determined via PCR chromosomal
CC   localisation using primers AAZ11934 and AAZ11936. K+Hnov cDNAs were
CC   isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple independent
CC   clones. Potassium channels have critical roles in various cell types and
CC   biochemical pathways. Defective potassium channels are known to cause
CC   four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
CC   (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
CC   channels are critical components of virtually all cells, it is likely
CC   that abnormal potassium channels are also implicated in certain renal,
CC   cardiovascular and central nervous system (CNS) disorders. Nucleotides
CC   encoding K+Hnov proteins may be used for identifying homologous or
CC   related proteins and the DNA sequences encoding them. They may be used to
CC   produce compositions that modulate the expression and function of the
CC   K+Hnov protein and in studying the biochemical pathways associated with
CC   it. They may also be used for the recombinant production of K+Hnov
CC   protein in fermentation cultures. Additionally, such nucleotides may be
CC   used in gene therapy protocols for the treatment of diseases associated
CC   with abnormal potassium channels
XX
SQ   Sequence 1246 BP; 345 A; 299 C; 302 G; 300 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              7.2e-46       Length:          1246
Score:                  481.50        Matches:         98
Percent Similarity:     60.43%        Conservative:    44
Best Local Similarity:  41.70%        Mismatches:      80
Query Match:            38.80%        Indels:          13
DB:                     2             Gaps:            5

US-09-914-053A-5 (1-235) x AAZ11912 (1-1246)

Qy          7 GlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGlnLysIleArg 26
              |||||||||:::                  ::::::         |||
Db        318 GGGAGGACAGCCTTTCCTGCCTCAGGGAAGAAGAGAGAGACAGACTACAGT--------- 368

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
              |||   |||   ||||||       |||   :::   :::      ||||||||||||||
Db        369 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTGCTGGAGAGGACCGA 425

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
              |||::::::||||||   |||||||||      |||::::::|||:::||||||||||||
Db        426 GCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 485

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
                 |||:::|||:::   :::|||   |||:::      |||||||||   ||||||
Db        486 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 545

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
              ::::::      |||   :::   :::   :::|||:::|||:::||||||      |||
Db        546 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 605

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
                  :::|||||||||||||||||||:::||||||||:::      |||:::
Db        606 CACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 665

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
              |||   ||||||::::::   ||||||   :::::|||||||   ||||||   |||
Db        666 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 725

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
              ||||||||          ::::::          |||:::|||      ::::::
Db        726 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 776

Qy        166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
                  :::   |||                |||||||||:::      |||
Db        777 AAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCAGCCAGC 836

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
                 :::   |||||||||   |||   |||              :::||||||   |||
Db        837 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 896

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||:::      :::   ||||||      ||||||   ||||||:::||||||
Db        897 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 956

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||:::||||||||||||||||:::         :::   |||
Db        957 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 1001

RESULT 9
ABA09433
ID   ABA09433 standard; cDNA; 558 BP.
XX
AC   ABA09433;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human K channel subunit homologue-encoding cDNA, SEQ ID NO:1209.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US003800.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
```

XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB12189.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 945; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 558 BP; 165 A; 128 C; 144 G; 121 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.46e-46	Length:	558
Score:	481.00	Matches:	94
Percent Similarity:	97.94%	Conservative:	1
Best Local Similarity:	96.91%	Mismatches:	2
Query Match:	38.76%	Indels:	0
DB:	4	Gaps:	0

US-09-914-053A-5 (1-235) x ABA09433 (1-558)

```
Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAGAGAAAT 327

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTACCAGAGAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 387

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        388 AAGGCAGGAGAGGACCGAGCTATTCTACTGGGACTGGCTATGATGGTGTGCTCCATCATG 447

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
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              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        448 ATGTAATTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCCGA 507

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCys 97
              ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        508 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGC 558
```

RESULT 10
AAF27992
ID AAF27992 standard; DNA; 1237 BP.
XX
AC AAF27992;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human calcium sensitive potassium channel beta3a subunit coding sequence.
XX
KW Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW irritable bowel syndrome; Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
PN WO200105828-A1.
XX
PD 25-JAN-2001.
XX
PF 18-JUL-2000; 2000WO-US019585.
XX
PR 20-JUL-1999; 99US-0144764P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Uebele V, Swanson R, Liu Y, Lagrutta A;
XX
DR WPI; 2001-159514/16.
DR P-PSDB; AAB35302.
XX
PT Novel human calcium sensitive potassium channel subunits for identifying
PT inhibitors and agonists of the potassium channel for use in treating
PT conditions such as asthma, hypertension, memory disorders, depression.
XX
PS Claim 3; Fig 2A; 89pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC and beta3d subunits. These can be used to identify inhibitors and
CC activators of the channels, which can be used in the treatment of
CC conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC incontinence, migraine and irritable bowel syndrome. The coding sequences
CC are found at human chromosome 3q23-ter. The present sequence is the
CC beta3a subunit coding sequence
XX
SQ Sequence 1237 BP; 314 A; 312 C; 324 G; 287 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1.6e-45	Length:	1237
Score:	478.50	Matches:	97
Percent Similarity:	60.00%	Conservative:	44
Best Local Similarity:	41.28%	Mismatches:	81
Query Match:	38.56%	Indels:	13
DB:	4	Gaps:	5

US-09-914-053A-5 (1-235) x AAF27992 (1-1237)

```
Qy          7 GlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGlnLysIleArg 26
              |||||||||:::          ::::::      |||
Db        398 GGGAGGACAGCCTTTCCTGCCTCAGGGAAGAAGAGAGACAGACTACAGT--------- 448

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
              |||  |||  ||||||     |||  :::  :::        ||||||||||||
```

```
Db        449 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTACTGGAGAGGACCGA 505

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
Db        506 GCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 565

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
Db        566 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 625

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
Db        626 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 685

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
Db        686 CACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 745

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
Db        746 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 805

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
Db        806 CCTAAGTGC---------CACCAAGATAGAAGTGATTTGCTCAACAGTGCTCTGGACATA 856

Qy        166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
Db        857 AAAGAATTCTTCGATCACAAAAATGGAACCCCCTTTTCATGCTTCTACAGTCCAGCCAGC 916

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
Db        917 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 976

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
Db        977 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 1036

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
Db       1037 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 1081
```

```
RESULT 11
AAZ11913
ID   AAZ11913 standard; cDNA; 1111 BP.
XX
AC   AAZ11913;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov44 cDNA (splice variant 2).
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             297. .959
FT                   /*tag=  a
FT                   /product= "Human K+Hnov44 potassium channel"
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US003826.
XX
PR   25-FEB-1998;   98US-0076687P.
PR   07-AUG-1998;   98US-0095836P.
PR   19-JAN-1999;   99US-0116448P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Miller AP,  Curran ME,  Hu P,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; AAY34131.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
PT   useful for the diagnosis and treatment of episodic ataxia with myokymia,
PT   cardiac arrhythmia, epilepsy and Bartter's syndrome.
XX
PS   Claim 4; Page 90-91; 112pp; English.
XX
CC   This sequence represents splice variant 2 of a human potassium channel
CC   K+Hnov44 cDNA. Alternative splicing does not affect the amino acid
CC   sequence of the protein. K+Hnov proteins have a high degree of homology
CC   to known potassium channels and may be alpha subunits, which form the
CC   functional channel, or accessory subunits that act to modulate the
CC   channel activity. K+Hnov44 is a potassium channel beta subunit. The
CC   gene's chromosomal location is 22p13, determined via PCR chromosomal
CC   localisation using primers AAZ11934 and AAZ11936. K+Hnov cDNAs were
CC   isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple independent
CC   clones. Potassium channels have critical roles in various cell types and
CC   biochemical pathways. Defective potassium channels are known to cause
CC   four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
CC   (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
CC   channels are critical components of virtually all cells, it is likely
CC   that abnormal potassium channels are also implicated in certain renal,
CC   cardiovascular and central nervous system (CNS) disorders. Nucleotides
CC   encoding K+Hnov proteins may be used for identifying homologous or
CC   related proteins and the DNA sequences encoding them. They may be used to
CC   produce compositions that modulate the expression and function of the
CC   K+Hnov protein and in studying the biochemical pathways associated with
CC   it. They may also be used for the recombinant production of K+Hnov
CC   protein in fermentation cultures. Additionally, such nucleotides may be
CC   used in gene therapy protocols for the treatment of diseases associated
CC   with abnormal potassium channels
XX
SQ   Sequence 1111 BP; 347 A; 237 C; 263 G; 264 T; 0 U; 0 Other;
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Alignment Scores:
Pred. No.:              1.55e-45      Length:          1111
Score:                  478.00        Matches:           94
Percent Similarity:     62.79%        Conservative:      41
Best Local Similarity:  43.72%        Mismatches:        70
Query Match:            38.52%        Indels:            10
DB:                     2             Gaps:               4

US-09-914-053A-5 (1-235) x AAZ11913 (1-1111)

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
Db        234 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTGCTGGAGAGGACCGA 290

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
Db        291 GCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 350

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
Db        351 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 410

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
Db        411 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 470

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
Db        471 CACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 530

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
```

```
Db        531 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 590

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
              |||||||||           ::::::         |||:::|||      ::::::
Db        591 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 641

Qy        166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
                    :::   |||               |||||||||:::      |||
Db        642 AAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCAGCCAGC 701

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
                  :::   |||||||||   |||   |||           :::||||||   |||
Db        702 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 761

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||:::      :::   ||||||      ||||||  ||||||:::||||||
Db        762 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 821

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||:::|||||||||||||||||||:::         :::   |||
Db        822 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 866

RESULT 12
AAK52128
ID   AAK52128 standard; cDNA; 1144 BP.
XX
AC   AAK52128;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 673.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78995.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 1; Page 2356-2357; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 1144 BP; 289 A; 296 C; 291 G; 268 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:                1.86e-45      Length:          1144
Score:                    477.50        Matches:         97
Percent Similarity:       60.00%        Conservative:    44
Best Local Similarity:    41.28%        Mismatches:      81
Query Match:              38.48%        Indels:          13
DB:                       4             Gaps:            5

US-09-914-053A-5 (1-235) x AAK52128 (1-1144)

Qy          7 GlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGlnLysIleArg 26
              |||||||||:::                 ::::::       |||
Db        371 GGGAGGACAGCCTTTCCTGCCTCAGGGAAGAAGAGAGACAGACTACAGT--------- 421

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
              |||   |||   ||||||      |||  :::  :::      ||||||||||||
Db        422 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTACTGGAGAGGACCGA 478

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
              |||::::::|||||    |||||||||       |||:::::|||:::|||||||||||
Db        479 GCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 538

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
                 |||:::|||:::   :::|||   |||:::      |||||||||   ||||||
Db        539 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 598

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
              ::::::      |||  :::   :::  :::|||:::|||:::||||||       |||
Db        599 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 658

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
                      :::|||||||||||||||||||:::|||||||||:::      |||:::
Db        659 CACGGTCAGGGGAAGTACCCATGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 718

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
              |||   ||||||:::::   ||||||   ::::::||||||   ||||||   |||
Db        719 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 778

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
              |||||||||                 ::::::         |||:::|||      ::::::
Db        779 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 829

Qy        166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
                    :::   |||               |||||||||:::      |||
Db        830 AAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCAGCCAGC 889

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
                  :::   |||||||||   |||   |||           :::||||||   |||
Db        890 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 949

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||:::      :::   ||||||      ||||||  ||||||:::||||||
Db        950 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 1009

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||:::|||||||||||||||||||:::         :::   |||
Db       1010 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 1054

RESULT 13
ABA09214
ID   ABA09214 standard; cDNA; 1251 BP.
XX
```

AC ABA09214;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human Ca-activated K channel homologue-encoding cDNA, SEQ ID NO:990.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB11970.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 843-844; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neurocepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a cDNA encoding a
CC novel human polypeptide of the invention
XX
SQ Sequence 1251 BP; 331 A; 304 C; 310 G; 306 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.12e-45	Length:	1251
Score:	477.50	Matches:	97
Percent Similarity:	60.00%	Conservative:	44
Best Local Similarity:	41.28%	Mismatches:	81
Query Match:	38.48%	Indels:	13
DB:	4	Gaps:	5

US-09-914-053A-5 (1-235) x ABA09214 (1-1251)

```
Qy          7 GlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGlnLysIleArg 26
              |||||||||:::                  ::::::         |||
Db        339 GGGAGGACAGCCTTTCCTGCCTCAGGGAAGAAGAGAGACAGACTACAGT--------- 389

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
              |||  |||  ||||||     |||  :::  :::          ||||||||||||
Db        390 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTACTGGAGAGGACCGA 446

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
              |||::::::||||||   |||||||||      |||::::::|||:::||||||||||||
Db        447 GCCGTGATGCTGGGGTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 506

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
                 |||:::|||:::   :::|||   |||:::       |||||||||   ||||||
Db        507 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 566

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
              ::::::      |||   :::   :::   :::|||:::|||:::||||||       |||
Db        567 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 626

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
                  :::|||||||||||||||||:::|||||||||:::      |||:::
Db        627 CACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 686

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
              |||   ||||||:::::   ||||||   :::::|||||   ||||||   |||
Db        687 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 746

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
              |||||||||           ::::::         |||:::|||      ::::::
Db        747 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 797

Qy        166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
                  :::   |||                 |||||||||:::      |||
Db        798 AAAGAATTCTTCGATCACAAAAATGGAACCCCCTTTTCATGCTTCTACAGTCCAGCCAGC 857

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
                 :::   |||||||||   |||   |||           :::||||||   |||
Db        858 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 917

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||:::     :::   ||||||      ||||||   ||||||:::||||||
Db        918 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 977

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||:::||||||||||||||||:::          :::   |||
Db        978 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 1022
```

RESULT 14
AAK53112
ID AAK53112 standard; cDNA; 1251 BP.
XX

```
AC   AAK53112;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 2641.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM79979.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 1; Page 4899-4900; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 1251 BP; 331 A; 304 C; 310 G; 306 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:              2.12e-45        Length:         1251
Score:                  477.50          Matches:        97
Percent Similarity:     60.00%          Conservative:   44
Best Local Similarity:  41.28%          Mismatches:     81
Query Match:            38.48%          Indels:         13
DB:                     4               Gaps:           5

US-09-914-053A-5 (1-235) x AAK53112 (1-1251)

Qy          7 GlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGlnLysIleArg 26
              |||||||||:::           ::::::        |||
Db        339 GGGAGGACAGCCTTTCCTGCCTCAGGGAAGAAGAGAGAGACAGACTACAGT--------- 389

Qy         27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
                 |||   |||   ||||||        |||   :::   :::          ||||||||||
Db        390 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTACTGGAGAGGACCGA 446

Qy         47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
              |||::::::||||||   |||||||||       |||:::::::|||:::||||||||||||
Db        447 GCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGTTCTTCTTGCTCGGA 506

Qy         67 IleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThrLeu 86
                 |||:::|||:::   :::|||   |||:::      |||||||||   ||||||
Db        507 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 566

Qy         87 LeuAsnAlaSerIleThrGluThrPhe---AsnCysSerPheSerCysGlyProAspCys 105
              ::::::      |||   :::   :::   :::|||:::|||:::||||||      |||
Db        567 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 626

Qy        106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
                       :::|||||||||||||||||:::|||||||||:::          |||:::
Db        627 CACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCAGCCATCCAGGTCAG 686

Qy        126 LysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyrIle 145
              |||   ||||||::::::   ||||||   :::::||||||   ||||||   |||
Db        687 AAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCAAGTGCTTTTACACA 746

Qy        146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
              |||||||||          ::::::          |||:::|||      ::::::
Db        747 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 797

Qy        166 PheArgLysTyrGlnHis----------------PheSerCysTyrSerAspProGluGly 180
                    :::   |||                 |||||||||:::      |||
Db        798 AAAGAATTCTTCGATCACAAAAATGGAACCCCCTTTTCATGCTTCTACAGTCCAGCCAGC 857

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              :::   |||||||||  |||   |||              :::||||||   |||
Db        858 CAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACTGTTTA 917

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||:::      :::   ||||||      ||||||   ||||||:::||||||
Db        918 TTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGATTAACA 977

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||:::||||||||||||||||||:::          :::   |||
Db        978 CAACACCTGTCCTTACTGTGTGAAAAATATAGCACTGTAGTCAGA 1022

RESULT 15
AAA75009
ID   AAA75009 standard; DNA; 774 BP.
XX
AC   AAA75009;
XX
DT   02-JAN-2001  (first entry)
XX
DE   DNA encoding a human BK beta-2 polypeptide.
XX
KW   Human; BK beta-2; beta subunit; Slo potassium channel; BK beta-3;
KW   BK beta-4; ion flux; migraine; hearing; vision problem; seizure; stroke;
KW   asthma; cell proliferation; hormone secretion; cancer; viral infection;
KW   ss.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .774
FT                   /*tag=  a
FT                   /product= "BK beta-2"
XX
PN   WO200050444-A1.
XX
PD   31-AUG-2000.
XX
PF   22-FEB-2000; 2000WO-US004441.
XX
PR   23-FEB-1999;   99US-0121224P.
PR   03-NOV-1999;   99US-0163367P.
```

XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ, Wickenden A, Liu Y;
XX
DR WPI; 2000-533179/48.
DR P-PSDB; AAB08818.
XX
PT Isolated beta subunit polynucleotides and polypeptides of Slo potassium
PT channels are used to determine the effects of compounds on ion flux
PT through a potassium channel and in computer modelling systems.
XX
PS Claim 7; Page 79; 84pp; English.
XX
CC The present sequence encodes a human BK beta-2 polypeptide. The
CC polypeptide is a beta subunit of a Slo potassium channel. The
CC specification also describes BK beta-3 and BK beta-4 polypeptides. BK
CC beta subunits are auxiliary subunits or monomers of Slo potassium
CC channels. The polypeptides, when expressed in cells and cell membranes,
CC are used to determine the effects of compounds on ion flux through a
CC potassium channel. The compounds identified may be useful as therapeutic
CC agents e.g. modulators that target specific Slo channels are useful for
CC treating migraines, hearing and vision problems, seizures, stroke,
CC asthma, cell proliferation and hormone secretion. The computer generated
CC 3-dimensional structures of BK beta 2, BK beta 3 or BK beta 4 are used to
CC identify ligands that bind to the beta subunit. The characterized BK beta
CC subunits are used to determine how Slo potassium channels function in
CC different environments and how they respond to different activation
CC mechanisms. The polynucleotides are used to transfect cells in vivo and
CC in vitro to mitigate effects of absent, partial inactivation or abnormal
CC expression of the BK beta subunit gene e.g. to correct genetic defects,
CC cancer and viral infection
XX
SQ Sequence 774 BP; 223 A; 177 C; 179 G; 195 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	2.65e-45	Length:	774
Score:	474.00	Matches:	93
Percent Similarity:	62.33%	Conservative:	41
Best Local Similarity:	43.26%	Mismatches:	71
Query Match:	38.20%	Indels:	10
DB:	3	Gaps:	4

US-09-914-053A-5 (1-235) x AAA75009 (1-774)

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Qy          27 AspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGlyGluAspArg 46
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Db          49 GATGGAGACCCACTAGATGTGCACAAGAGGCTGCCATCC---AGTACTGGAGAGGACCGA 105

Qy          47 AlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeuLeuGly 66
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Db         166 ACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAATCGACCTGCACTGCC 225

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               ::::::      |||   :::   :::   :::|||:::|||:::||||||      |||
Db         226 ATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCTGTGGTGTGCACTGC 285

Qy         106 TrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGlyGlu 125
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Qy         146 ProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGluAsn 165
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Db         406 CCTAAGTGC---------CACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGGACATA 456

Qy         166 PheArgLysTyrGlnHis--------------PheSerCysTyrSerAspProGluGly 180
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Qy         181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
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Qy         201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Qy         221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
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Search completed: November 7, 2004, 01:38:40
Job time : 412 secs

GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 23:31:06 ; Search time 3203 Seconds
(without alignments)
10438.282 Million cell updates/sec

Title: US-09-914-053A-6
Perfect score: 707
Sequence: 1 atgtcgatatggaccagtgg.....atccacggatcaatagataa 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
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11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	692	97.9	1075	9	AF099137	AF099137 Homo sapi
	2	692	97.9	1285	9	BC017825	BC017825 Homo sapi
	3	692	97.9	2574	9	AF209747	AF209747 Homo sapi
	4	666	94.2	1062	6	CQ714334	CQ714334 Sequence
	5	567.2	80.2	708	10	AY062429	AY062429 Mus muscu
	6	567.2	80.2	2947	10	BC046227	BC046227 Mus muscu
	7	567.2	80.2	2947	10	BC058957	BC058957 Mus muscu
	8	564.2	79.8	2098	6	BD223084	BD223084 98 human
	9	564.2	79.8	2098	6	AR243782	AR243782 Sequence
	10	562.4	79.5	708	10	AY191836	AY191836 Rattus no
	11	438.4	62.0	1546	5	BX950825	BX950825 Gallus ga
	12	438.4	62.0	1546	5	BX950833	BX950833 Gallus ga
	13	384.4	54.4	487	10	RNO517198	AJ517198 Rattus no
	14	274.8	38.9	204899	9	AC117457	AC117457 Homo sapi
	15	229.8	32.5	191186	2	AC115077	AC115077 Mus muscu
c	16	225	31.8	227094	2	AC126508	AC126508 Rattus no
	17	225	31.8	297398	2	AC097578	AC097578 Rattus no
	18	193.6	27.4	815	5	CCU67865	U67865 Coturnix co
	19	193.6	27.4	826	5	AF077369	AF077369 Gallus ga
	20	193.6	27.4	1290	5	AF420468	AF420468 Gallus ga
c	21	151.2	21.4	270878	2	AC114433	AC114433 Rattus no
c	22	145.8	20.6	191186	2	AC115077	AC115077 Mus muscu
	23	140.6	19.9	622	11	G97798	G97798 S209P6139FA
	24	135.4	19.2	1022	6	CQ715541	CQ715541 Sequence
	25	135.4	19.2	1111	6	AR212368	AR212368 Sequence
	26	135.4	19.2	1246	6	AR212367	AR212367 Sequence
	27	134.4	19.0	952	9	AF214561	AF214561 Homo sapi
	28	134.4	19.0	1022	9	AF139471	AF139471 Homo sapi
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	30	134.4	19.0	1225	9	AF204159	AF204159 Homo sapi
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	34	134.4	19.0	1747	9	AF204161	AF204161 Homo sapi
	35	134	19.0	576	9	AF026002	AF026002 Homo sapi
	36	134	19.0	576	9	HSU38907	U38907 Human beta-
	37	134	19.0	715	9	AY044441	AY044441 Homo sapi
	38	134	19.0	835	9	AY515264	AY515264 Homo sapi
	39	134	19.0	1041	9	HSU42600	U42600 Human calci
	40	134	19.0	1092	9	HSU61536	U61536 Human potas
	41	134	19.0	1106	6	AR016453	AR016453 Sequence
	42	134	19.0	1106	6	I45572	I45572 Sequence 3
	43	134	19.0	1276	6	CQ726048	CQ726048 Sequence
	44	134	19.0	1277	6	AX337509	AX337509 Sequence
	45	134	19.0	1277	9	HSU25138	U25138 Human MaxiK

ALIGNMENTS

RESULT 1
AF099137
LOCUS AF099137 1075 bp mRNA linear PRI 06-APR-1999
DEFINITION Homo sapiens MaxiK channel beta 2 subunit (KCNMB2) mRNA, complete cds.
ACCESSION AF099137
VERSION AF099137.1 GI:4566496
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS Wallner,M., Meera,P. and Toro,L.
TITLE Molecular basis of fast inactivation in voltage and Ca2+-activated K+ channels: a transmembrane beta-subunit homolog
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 4137-4142 (1999)
MEDLINE 99199323
PUBMED 10097176
REFERENCE 2 (bases 1 to 1075)
AUTHORS Wallner,M.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Dept. of Anesthesiology, UCLA, BH-612, CHS Box 951778, Los Angeles, CA 90095-1778, USA
FEATURES Location/Qualifiers
source 1. .1075
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/db_xref="taxon:9606"
/clone="IMAGE Consortium ID 1417217"
/tissue_type="neuroendocrine lung carcinoid"
gene 1. .1075
/gene="KCNMB2"
CDS 146. .853
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/codon_start=1
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ORIGIN

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  Best Local Similarity   99.3%;  Pred. No. 2.3e-194;
  Matches  703;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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RESULT 2

```
BC017825
LOCUS       BC017825                1285 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens potassium large conductance calcium-activated channel,
            subfamily M, beta member 2, transcript variant 1, mRNA (cDNA clone
            MGC:22431 IMAGE:4657825), complete cds.
ACCESSION   BC017825
VERSION     BC017825.1  GI:17389593
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1285)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1285)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAL Plate: 36 Row: i Column: 8
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 19923319.
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ORIGIN

  Query Match             97.9%;  Score 692;  DB 9;  Length 1285;
  Best Local Similarity   99.3%;  Pred. No. 2.3e-194;
  Matches  703;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
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RESULT 3
AF209747

LOCUS       AF209747               2574 bp    mRNA    linear   PRI 29-FEB-2000
DEFINITION  Homo sapiens large conductance calcium-activated potassium channel
            beta2 subunit (KCNMB2) mRNA, complete cds.
ACCESSION   AF209747
VERSION     AF209747.1  GI:7108972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2574)
  AUTHORS   Brenner,R., Jegla,T.J., Wickenden,A., Liu,Y. and Aldrich,R.W.
  TITLE     Cloning and functional characterization of novel large conductance
            calcium-activated potassium channel beta subunits, hKCNMB3 and
            hKCNMB4
  JOURNAL   J. Biol. Chem. 275 (9), 6453-6461 (2000)
  MEDLINE   20158960
   PUBMED   10692449
REFERENCE   2  (bases 1 to 2574)
  AUTHORS   Brenner,R., Jegla,T.J., Wickenden,A., Liu,Y. and Aldrich,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1999) Molecular and Cell Physiology, Howard
            Hughes Medical Institute, Stanford School of Medicine, Beckman
            B173, Stanford, CA 94305, USA
FEATURES             Location/Qualifiers
     source          1. .2574
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /tissue_type="ovary"
     gene            1. .2574
                     /gene="KCNMB2"
     CDS             353. .1060
                     /gene="KCNMB2"
                     /note="hKCNMB2; large conductance (BK) potassium channel
                     beta2 subunit"
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                     /product="large conductance calcium-activated potassium
                     channel beta2 subunit"
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ORIGIN

  Query Match             97.9%;  Score 692;  DB 9;  Length 2574;
  Best Local Similarity   99.3%;  Pred. No. 2.4e-194;
  Matches  703;  Conservative    2;  Mismatches    2;  Indels    1;  Gaps    1;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db        353 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 412

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        413 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 472

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        473 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 532

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        593 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 652

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        653 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 712

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Db        713 ACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 772

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Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Db        833 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 892

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Db        893 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 952

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
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Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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RESULT 4
CQ714334
LOCUS CQ714334 1062 bp DNA linear PAT 03-FEB-2004
DEFINITION Sequence 268 from Patent WO02068579.
ACCESSION CQ714334
VERSION CQ714334.1 GI:42275191
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
TITLE Kits, such as nucleic acid arrays, comprising a majority of humanexons or transcripts, for detecting expression and other uses thereof
JOURNAL Patent: WO 02068579-A 268 06-SEP-2002;
PE Corporation (NY) (US)
FEATURES Location/Qualifiers
source 1. .1062
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN

Query Match 94.2%; Score 666; DB 6; Length 1062;
Best Local Similarity 99.1%; Pred. No. 1.2e-186;
Matches 688; Conservative 2; Mismatches 2; Indels 2; Gaps 2;

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Db        147 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 206

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCT-GGACAAAAGGAAAACAGTCACAGCACT 119
                |||||||||||||||||||||||||||||| |||||||||||||||||||||||||||||||
Db        207 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGGACAAAAGGAAAACAGTCACAGCACT 266

Qy        120 GAAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCAT 179
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Db        267 GAAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCAT 326

Qy        180 GATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGA 239
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Db        327 GATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGA 386

Qy        240 AGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAG 299
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Db        387 AGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAG 446

Qy        300 CTGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCT 359
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Db        447 CTGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCT 506

Qy        360 GACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCA 419
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Db        507 GACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCA 566

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Db        567 GAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAA 626

Qy        480 TGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGG 539
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Db        627 TGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGG 686

Qy        540 AAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACT 599
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Db        687 AAACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACT 746

Qy        600 CTTCTGGCCAACCTGTATGATGGCT-GGGGGTGTGGCAATTGTTGCCATGGTGAAACTTA 658
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Db        747 CTTCTGGCCAACCTGTATGATGGCTGGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTA 806

Qy        659 CACAGTACCTCTCCCTACTATGTGAGAGGATCCA 692
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RESULT 5
AY062429
LOCUS AY062429 708 bp mRNA linear ROD 12-DEC-2001
DEFINITION Mus musculus large conductance calcium-activated K channel beta2 subunit mRNA, complete cds.
ACCESSION AY062429
VERSION AY062429.1 GI:17644138
KEYWORDS .
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 708)
AUTHORS Garcia-Valdes,J., Eghbali,M., Stefani,E. and Toro,L.
TITLE Mouse kcnmb2 subunit of the large conductance calcium-activated K channel (MaxiK, BK)
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 708)
AUTHORS Garcia-Valdes,J., Eghbali,M., Stefani,E. and Toro,L.
TITLE Direct Submission
JOURNAL Submitted (14-NOV-2001) Anesthesiology, UCLA, PO Box 957115, BH-509A CHS, Los Angeles, CA 90095-7115, USA
FEATURES Location/Qualifiers
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/mol_type="mRNA"
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/dev_stage="fetus"
CDS 1. .708
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/codon_start=1
/product="large conductance calcium-activated K channel beta2 subunit"
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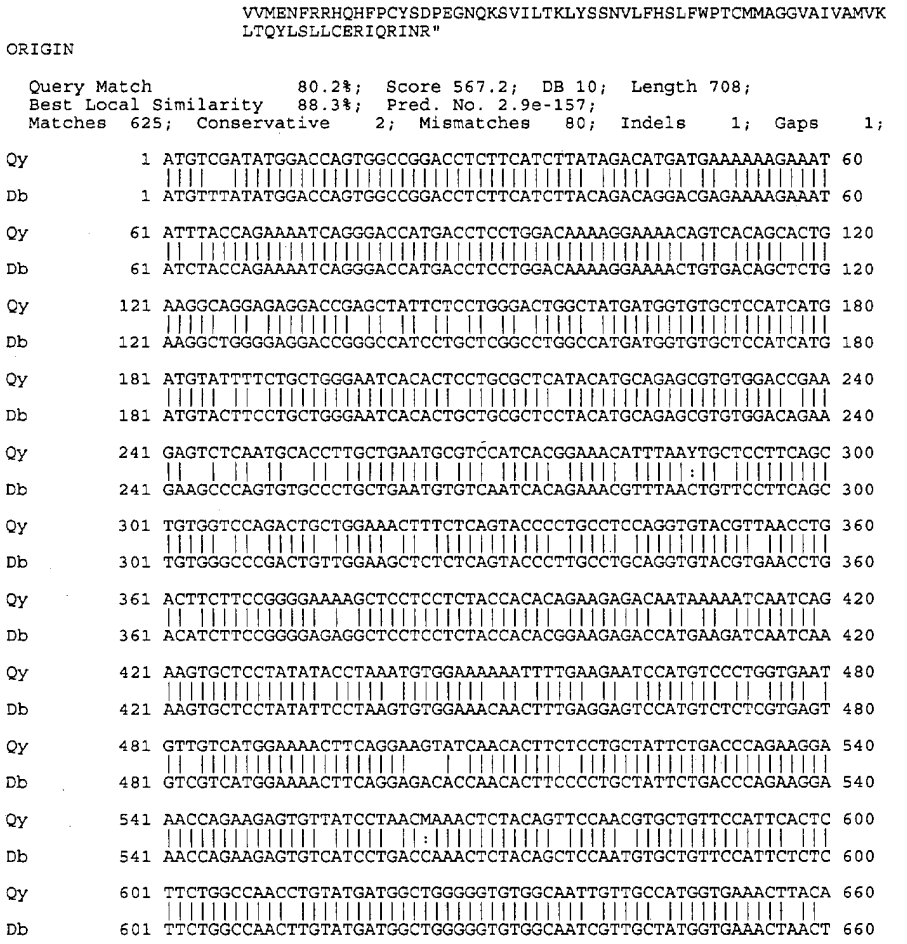
LTQYLSLLCERIQRINR"
ORIGIN

Query Match 80.2%; Score 567.2; DB 10; Length 708;
Best Local Similarity 88.3%; Pred. No. 2.9e-157;
Matches 625; Conservative 2; Mismatches 80; Indels 1; Gaps 1;



RESULT 6
BC046227
LOCUS BC046227 2947 bp mRNA linear ROD 30-JUN-2004
DEFINITION Mus musculus potassium large conductance calcium-activated channel, subfamily M, beta member 2, mRNA (cDNA clone MGC:57945 IMAGE:5703879), complete cds.
ACCESSION BC046227
VERSION BC046227.1 GI:28279339
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2947)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 2947)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (31-JAN-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr. Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312299.
FEATURES Location/Qualifiers
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/db_xref="taxon:10090"
/clone="MGC:57945 IMAGE:5703879"
/tissue_type="Brain, mouse 15.5 dpc"
/clone_lib="NIH_BMAP_EW0"
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CDS 391. .1098
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/product="potassium large conductance calcium-activated channel, subfamily M, beta member 2"
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LTQYLSLLCERIQRINR"

ORIGIN

Query Match 80.2%; Score 567.2; DB 10; Length 2947;
Best Local Similarity 88.3%; Pred. No. 3.3e-157;
Matches 625; Conservative 2; Mismatches 80; Indels 1; Gaps 1;

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Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db        391 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 450

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Db        451 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 510

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||| || |||||||| || || || || || ||||| ||||||||||||||||||||||
Db        511 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 570

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Db        571 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 630

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        631 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 690

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        691 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 750

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Db        811 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 870

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Db        991 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 1050

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db       1051 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGATAA 1098
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RESULT 7
BC058957
LOCUS BC058957 2947 bp mRNA linear ROD 30-JUN-2004
DEFINITION Mus musculus potassium large conductance calcium-activated channel, subfamily M, beta member 2, mRNA (cDNA clone MGC:66775 IMAGE:5703879), complete cds.
ACCESSION BC058957
VERSION BC058957.1 GI:37589334
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2947)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 2947)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Dr. Jim Lin, University of Iowa
cDNA Library Preparation: M. Bento Soares, University of Iowa
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Genome Sequence Centre,
BC Cancer Agency, Vancouver, BC, Canada
info@bcgsc.bc.ca
Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield, Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao, Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin, Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu, Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska, Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie Schein, Asim Siddiqui, Rob Holt, Marco Marra.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: IRAK Plate: 124 Row: i Column: 16
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312299.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
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gene 1. .2947
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ORIGIN

  Query Match             80.2%;  Score 567.2;  DB 10;  Length 2947;
  Best Local Similarity   88.3%;  Pred. No. 3.3e-157;
  Matches  625;  Conservative    2;  Mismatches   80;  Indels    1;  Gaps    1;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db        391 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 450

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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        511 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 570

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Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        631 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 690

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        691 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 750

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Db        751 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 810

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Db        871 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 930

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Db        931 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 990

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Db        991 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 1050

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db       1051 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGATAA 1098


RESULT 8
BD223084
LOCUS       BD223084                2098 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  98 human secretory proteins.
ACCESSION   BD223084
VERSION     BD223084.1  GI:33032854
KEYWORDS    JP 2002521055-A/19.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A.,
            Shi,Y., Lafleur,D., Wei,Y.F., Ni,J., Florence,K.A., Young,P.E.,
            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H.S. and
            Mucenski,M.
  TITLE     98 human secretory proteins
  JOURNAL   Patent: JP 2002521055-A 19 16-JUL-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002521055-A/19
            PD   16-JUL-2002
            PF   29-JUL-1999 JP 2000562480
            PR   30-JUL-1998 US    60/094657,05-AUG-1998 US    60/095486 PR
            06-AUG-1998 US    60/095455,06-AUG-1998 US    60/095454 PR
            12-AUG-1998 US    60/096319
            PI   GEORGE A KOMATSOULIS,CRAIG A ROSEN,STEVEN
            M RUBEN,ROXANNE DUAN,
            PI   PAUL A MOORE,YANGGU SHI,DAVID LAFLEUR,YING FEI WEI,JIAN NI, PI
              KIMBERLY A FLORENCE,PAUL E YOUNG,LAURIE A BREWER,DANIEL R  PI
            SOPPET,
            PI   GREGORY A ENDRESS,REINHARD EBNER,HENRIK S OLSEN,MICHAEL  PI
            MUCENSKI
            PC   C12N15/09,A61K31/713,A61K38/00,A61K48/00,C07K14/47,C07K16/18,
            PC   C12N1/15,
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            C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/68,G01N33/ PC
             15,
            PC
            G01N33/50,G01N33/53//A61P1/18,A61P5/02,A61P5/06,A61P5/14,A61P9/ PC
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            PC   A61P25/24,
            PC   A61P25/28,A61P27/02,A61P29/00,A61P31/18,A61P35/02,C12N15/00,
            PC   C12N5/00,
            PC   A61K37/02
            CC   98 human secretory proteins
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            FT   source          1. .2098
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match             79.8%;  Score 564.2;  DB 6;  Length 2098;
  Best Local Similarity   99.5%;  Pred. No. 2.5e-156;
  Matches  574;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

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Qy        492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
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RESULT 9
AR243782
LOCUS       AR243782               2098 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 20 from patent US 6476195.
ACCESSION   AR243782
VERSION     AR243782.1  GI:27291275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Komatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A.,
            Shi,Y., LaFleur,D.W., Wei,Y.-F., Ni,J., Florence,K.A., Young,P.,
            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H. and
            Mucenski,M.
  TITLE     Secreted protein HNFGF20
  JOURNAL   Patent: US 6476195-A 20 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .2098
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ORIGIN

  Query Match           79.8%;  Score 564.2;  DB 6;  Length 2098;
  Best Local Similarity   99.5%;  Pred. No. 2.5e-156;
  Matches  574;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        132 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 191
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Qy        192 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 251
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Db        249 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 308

Qy        432 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 491
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Qy        492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
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Db        369 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 428

Qy        552 TGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 611
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Db        429 TGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 488

Qy        612 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 671
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Db        489 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 548

Qy        672 CCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db        549 CCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 585


RESULT 10
AY191836
LOCUS       AY191836               708 bp    mRNA    linear   ROD 26-FEB-2003
DEFINITION  Rattus norvegicus inactivating beta 2 subunit of large conductance
            Ca2+-activated K+ channel mRNA, complete cds.
ACCESSION   AY191836
VERSION     AY191836.1  GI:28565441
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Eghbali,M., Foroughi,S., Toro,L. and Stefani,E.
  TITLE     Rat inactivating beta 2 subunit of large conductance Ca2+-activated
            K+ channel (KCNMB2, rSlo beta 2 subunit)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 708)
  AUTHORS   Eghbali,M., Foroughi,S., Toro,L. and Stefani,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Anesthesiology, UCLA, PO Box 957115, Room
            BH-509A CHS, Los Angeles, CA 90095-7115, USA
FEATURES             Location/Qualifiers
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ORIGIN

  Query Match           79.5%;  Score 562.4;  DB 10;  Length 708;
  Best Local Similarity   87.9%;  Pred. No. 7.8e-156;
  Matches  622;  Conservative    2;  Mismatches   83;  Indels    1;  Gaps    1;
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Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db          1 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACACGACGAGAAAAGAAAT 60

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              ||||| || |||||||||| || |||||||||| ||||| ||||| ||||| ||||||
Db        301 TGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAACCTG 360

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Db        361 ACATCTTCTGGGGAGAAGCTCCTCCTCTACCACACAGAAGAGACCATGAAGATCAATCAA 420

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Db        421 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCCCTTGTGAGT 480

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              || |||||||||||||||||    | |||||||| ||||||||||||||||||||||||||
Db        481 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGG 540

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              ||||| ||||| || ||||| ||:|||||||| || |||||| |||||||||||||| |||
Db        541 AACCAAAAGAGCGTCATCCTGACCAAACTCTATAGCTCCAATGTGCTGTTCCATTCTCTC 600

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              |||||||||||| |||||||||||||||||||||||||||||| ||||| |||||||||| ||
Db        601 TTCTGGCCAACGTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 660

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||| || |||||||||||||| |||||||| ||||||
Db        661 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGATAA 708
```

RESULT 11
BX950825
LOCUS BX950825 1546 bp mRNA linear VRT 17-FEB-2004
DEFINITION Gallus gallus finished cDNA, clone ChEST48b4.
ACCESSION BX950825
VERSION BX950825.1 GI:42600510
KEYWORDS .
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 1546)
AUTHORS Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E., Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V., Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R., Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G., Tickle,C. and Wilson,S.A.
TITLE Direct Submission
JOURNAL Submitted (16-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire, CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
COMMENT BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA sequencing project.
This sequence is from the
BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection, from a library constructed by Elizabeth Bosch. cDNA was prepared from RNA extracted from whole embryo, normalised, and poly A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector. Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host: Escherichia coli DH10B.
FEATURES Location/Qualifiers
source 1. .1546
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST48b4"
/clone_lib="CSEQCHN04"
/dev_stage="stage 10"
ORIGIN

Query Match 62.0%; Score 438.4; DB 5; Length 1546;
Best Local Similarity 78.5%; Pred. No. 6.5e-119;
Matches 556; Conservative 2; Mismatches 128; Indels 22; Gaps 2;

```
Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  || ||||||||||||||||| |||| |||||| ||||| ||||| |||
Db        144 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 197

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
                         |||||  || ||  || |||||||||||||||||||||||||||  ||
Db        198 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 242

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              || ||  ||||| |||||  || |||||  || |||||  |||||||||||||||| ||||||
Db        243 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 302

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||| ||||| |||||||||||  || |||||  || |||||||||||||||  ||||| |||
Db        303 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 362

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||| |||| ||| |  | || || || |||||||| |||||  || ||:||||| || |||
Db        363 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 422

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              || || |||||||||||||||| | ||||||||||||||||||  |||||||||||  || ||
Db        423 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 482

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |||||||  ||  | |||||  || ||||||||||  |||||  |||||  ||||| |||
Db        483 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 542

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              ||||  || ||  |||||  |||||  ||  ||||||||||  |||||||
Db        543 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 602

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              |||||  |||||||||||| | |||||||||  ||||||||||  | |||  || ||  ||
Db        603 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 662

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              |  |||||||  || ||  | ||:|||||  |||||  ||||||||||||||||||  || |||
Db        663 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 722

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              |||||||  || ||  |||||    || ||  ||  || ||||||||  |||||  || ||  ||
Db        723 TTCTGGCCCACGTGCATGATGATCGGCGGCGTTGCCATTGTTGCGATGGTAAAGCTGACT 782

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              || |||||  ||  ||  ||  ||  |||||  ||||  | |||||||  ||||||
Db        783 CAATACCTTTCTCTCCTCTGCGAGAGAATCCAAAGGATCAACAGATAA 830
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RESULT 12
BX950833
LOCUS BX950833 1546 bp mRNA linear VRT 30-MAR-2004

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DEFINITION  Gallus gallus finished cDNA, clone ChEST43b24.
ACCESSION   BX950833
VERSION     BX950833.2  GI:46019324
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
            Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
            Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
            Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
            Tickle,C. and Wilson,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
COMMENT     On Apr 1, 2004 this sequence version replaced gi:42600518.
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
            sequencing project.
            This sequence is from the
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
            from a library constructed by Elizabeth Bosch. cDNA was prepared
            from RNA extracted from whole embryo, normalised, and poly
            A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector.
            Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host:
            Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .1546
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="ChEST43b24"
                     /clone_lib="CSEQCHN04"
                     /dev_stage="stage 10"
ORIGIN

  Query Match             62.0%;  Score 438.4;  DB 5;  Length 1546;
  Best Local Similarity   78.5%;  Pred. No. 6.5e-119;
  Matches  556;  Conservative    2;  Mismatches  128;  Indels   22;  Gaps    2;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  || |||||||||||||||| |||| ||||||| ||||| ||||| |||
Db        144 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 197

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
                        ||||| || || || |||||||||||||||||||||||||| ||
Db        198 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 242

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              || || ||||| ||||| || || ||||| || ||||| |||||||||||||| ||||||
Db        243 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 302

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||| ||||| |||||||||| || ||||| || |||||||||||||| ||||| |||
Db        303 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 362

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||| |||| ||| |  | || || || |||||||| ||||| || ||:||||| || |||
Db        363 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 422

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              || || |||||||||||||| | |||||||||||||||| |||||||||| || ||
Db        423 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 482

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |||||||| ||  | ||||| || |||||||||| ||||| ||||| ||||| |||
Db        483 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 542

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              ||||  || || ||||| || ||||| || ||||  || |||||||||||  |||||||

Db        543 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 602

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              ||||| |||||||||||| | |||||||||| |||||||||||  | ||| || || ||
Db        603 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 662

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              |  |||||||  || ||  | ||:||||| ||||| |||||||||||||||||| || |||
Db        663 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 722

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              |||||||| || || ||||||   || || || || |||||||| ||||| || || ||
Db        723 TTCTGGCCCACGTGCATGATGATCGGCGGCGTTGCCATTGTTGCGATGGTAAAGCTGACT 782

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              || ||||| || || || || ||||| |||| | |||||||| ||||||
Db        783 CAATACCTTTCTCTCCTCTGCGAGAGAATCCAAAGGATCAACAGATAA 830


RESULT 13
RNO517198
LOCUS       RNO517198               487 bp    mRNA    linear   ROD 15-DEC-2002
DEFINITION  Rattus norvegicus partial mRNA for calcium-activated potassium
            channel beta 2 subunit (Kcnmb2 gene).
ACCESSION   AJ517198
VERSION     AJ517198.1  GI:26801163
KEYWORDS    calcium-activated potassium channel beta 2 subunit; Kcnmb2 gene.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1
  AUTHORS   Langer,P., Grunder,S. and Rusch,A.
  TITLE     Expression of Ca2+-activated BK channel mRNA and its splice
            variants in the rat cochlea
  JOURNAL   J. Comp. Neurol. 455 (2), 198-209 (2003)
  MEDLINE   22342043
   PUBMED   12454985
REFERENCE   2  (bases 1 to 487)
  AUTHORS   Langer,P.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-NOV-2002) Langer P., Institute of Physiology II,
            University of Tuebingen, Gmelinstr. 5, Tuebingen, D-72076, GERMANY
FEATURES             Location/Qualifiers
     source          1. .487
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /strain="Wistar"
                     /db_xref="taxon:10116"
                     /tissue_type="brain"
     gene            1. .487
                     /gene="Kcnmb2"
     CDS             <1. .>487
                     /gene="Kcnmb2"
                     /function="ion channel"
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                     /product="calcium-activated potassium channel beta 2
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                     /protein_id="CAD56888.1"
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                     CSYIPKCGNNFEESMSLVSVVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHS
                     LF"
ORIGIN

  Query Match             54.4%;  Score 384.4;  DB 10;  Length 487;
  Best Local Similarity   86.6%;  Pred. No. 6.8e-103;
  Matches  421;  Conservative    2;  Mismatches   63;  Indels    0;  Gaps    0;
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```
Qy        118 CTGAAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATC 177
              ||||||||  ||||||||||  ||  ||  ||  ||  ||||||||  ||||||||||||||||||
Db          2 CTGAAGGCTGGAGAGGACCGGGCCATCCTGCTTGGACTGGCCATGATGGTGTGCTCCATC 61

Qy        178 ATGATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACC 237
              ||||||||  ||  ||  ||||||||||||||||  ||||||||  ||||||||||  ||||||||
Db         62 ATGATGTACTTCCTACTGGGAATCACACTGCTGCGCTCGTACATGCAGAGTGTGTGGACA 121

Qy        238 GAAGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTC 297
              |||||  |  ||  ||  ||  |||||||||  |||  |||||  ||||||||||:||  ||||||
Db        122 GAAGAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACATTTAACTGTTCCTTC 181

Qy        298 AGCTGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAAC 357
              ||||||||  ||  ||||||||||  ||  ||||||||||  |||||  |||||  |||  |||
Db        182 AGCTGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAAC 241

Qy        358 CTGACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAAT 417
              |||||  |||||  |||||  ||||||||||||||||||||||||||||||  ||  ||||||
Db        242 CTGACATCTTCTGGGGAGAAGCTCCTCCTCTACCACACAGAAGAGACCATGAAGATCAAT 301

Qy        418 CAGAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTG 477
              ||  ||||||||||||||  |||||  ||||||||  ||  |||||  ||  ||||||||||  |||
Db        302 CAAAAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCCCTTGTG 361

Qy        478 AATGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAA 537
              |  |||  ||||||||||||||||||||  |  |||||||||  ||||||||||||||||||
Db        362 AGTGTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAA 421

Qy        538 GGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCA 597
              ||  |||||  |||||  ||  |||||  ||:||||||||  ||  |||||  ||||||||||||||
Db        422 GGGAACCAAAAGAGCGTCATCCTGACCAAACTCTATAGCTCCAATGTGCTGTTCCATTCT 481

Qy        598 CTCTTC 603
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Db        482 CTCTTC 487
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RESULT 14
AC117457

```
LOCUS       AC117457               204899 bp    DNA     linear   PRI 25-FEB-2003
DEFINITION  Homo sapiens 3 BAC RP11-385J1 (Roswell Park Cancer Institute Human
            BAC Library) complete sequence.
ACCESSION   AC117457
VERSION     AC117457.11  GI:28557825
KEYWORDS    HTG.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 204899)
  AUTHORS   Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C.,
            Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T.,
            Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D.,
            Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P.,
            Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C.,
            Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D.,
            Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C.,
            Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R.,
            Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A.,
            Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H.,
            Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J.,
            Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M.,
            Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P.,
            Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R.,
            Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K.,
            Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X.,
            Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,
            Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J.,
            Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S.,
            Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J.,
            Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C.,
            Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W.,
            Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R.,
            Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A.,
            Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M.,
            Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K.,
            Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D.,
            Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N.,
            Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N.,
            Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L.,
            Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M.,
            Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S.,
            Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E.,
            Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A.,
            Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C.,
            Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L.,
            Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S.,
            Warren,R., Washington,C., Watlington,S., Williams,G.,
            Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y.,
            Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and
            Gibbs,R.
  TITLE     Direct Submission
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 204899)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-APR-2002) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   3  (bases 1 to 204899)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (22-FEB-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
REFERENCE   4  (bases 1 to 204899)
  AUTHORS   Worley,K.C.
  TITLE     Direct Submission
  JOURNAL   Submitted (25-FEB-2003) Human Genome Sequencing Center, Department
            of Molecular and Human Genetics, Baylor College of Medicine, One
            Baylor Plaza, Houston, TX 77030, USA
COMMENT     On Feb 25, 2003 this sequence version replaced gi:28467084.
            INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email
            gc-help@bcm.tmc.edu

            CLONE LENGTH: This sequence does not necessarily represent the
            entire insert of this clone. Overlapping regions of clones are only
            sequenced and submitted once, so the sequence for the remainder of
            the insert may be found in the record for the adjacent clones.
            Overlapping clones are noted at the beginning and end of the
            Features listing.

            ANNOTATION OF FEATURES:
               STSs are identified using ePCR (Genome Res. 7:541-550) searches
            of a local database that includes entries from dbSTS, GDB, and
            local mapping efforts.
               Repeats are identified using RepeatMasker (A. Smit and P. Green,
            unpublished.) for Human and Mouse sequences.
               Genes and Region of sequence similarity are identified by BLAST
            (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the
            EST and cDNA sequences. Genes demonstrate at least two exons
            flanked by consensus splice sites that maintained sequence
            continuity across the splice junctions. Sequences that are not
            identical matches are annotated as similar.

            SEQUENCING READ COVERAGE:Sequencing is completed to a minimum
            standard of double strand coverage with a minimum of 2 clones and 2
            reads with no ambiguities or 2 chemistries with a minimum of 2
            clones and 3 reads with no ambiguities. If the sequence quality for
            a region does not meet this standard, it will be indicated in the
            annotation as Low Coverage.

            QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality
            standards - estimated error rate less than 1 per 10,000 bases.
            Reports of lowest quality individual bases and measures of base
            quality are listed below. Description of the metrics can be found
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          at URL:
          http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.ht
          ml.
FEATURES             Location/Qualifiers
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Qy        417 TCAGAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGT 476
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Qy        477 GAATGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGA 536
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Qy        537 AGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTC 596
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Qy        597 ACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACT 656
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Qy        657 TACACAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db     177714 TACACAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 177765


RESULT 15
AC115077
LOCUS       AC115077              191186 bp    DNA     linear   HTG 10-JUN-2002
DEFINITION  Mus musculus clone RP24-455M3, WORKING DRAFT SEQUENCE, 20 ordered
            pieces.
ACCESSION   AC115077
VERSION     AC115077.2  GI:21362205
KEYWORDS    HTG; HTGS_PHASE2; HTGS_DRAFT; HTGS_FULLTOP.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 191186)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C. and Lander,E.
  TITLE     Mus musculus, clone RP24-455M3
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 191186)
  AUTHORS   Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N.,
            Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L.,
            Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J.,
            Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A.,
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            Faro,S., Ferreira,P., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S.,
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TITLE Direct Submission

JOURNAL Submitted (14-MAR-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

REFERENCE 3 (bases 1 to 191186)

AUTHORS Birren,B., Linton,L., Nusbaum,C., Lander,E., Ali,A., Allen,N., Anderson,S., Barna,N., Bastien,V., Bloom,T., Boguslavkiy,L., Boukhgalter,B., Brown,A., Camarata,J., Campopiano,A., Chang,J., Chazaro,B., Choepel,Y., Colangelo,M., Collins,S., Collymore,A., Cook,A., Cooke,P., DeArellano,K., Dewar,K., Diaz,J.S., Dodge,S., Faro,S., Ferreira,P., FitzGerald,M., FitzHugh,W., Gage,D., Galagan,J., Gardyna,S., Ginde,S., Gord,S., Goyette,M., Graham,L., Grand-Pierre,N., Hagos,B., Horton,L., Hulme,W., Iliev,I., Johnson,R., Jones,C., Kamat,A., Karatas,A., Kells,C., LaRocque,K., Lamazares,R., Landers,T., Lehoczky,J., Levine,R., Lindblad-Toh,K., Liu,G., MacLean,C., Macdonald,P., Major,J., Marquis,N., Matthews,C., McCarthy,M., McEwan,P., McKernan,K., Meldrim,J., Meneus,L., Mihova,T., Mlenga,V., Murphy,T., Naylor,J., Nguyen,C., Nicol,R., Norbu,C., Norman,C.H., O'Connor,T., O'Donnell,P., O'Neil,D., Oliver,J., Peterson,K., Phunkhang,P., Pierre,N., Pollara,V., Raymond,C., Retta,R., Rieback,M., Riley,R., Rise,C., Rogov,P., Roman,J., Rosetti,M., Roy,A., Santos,R., Schauer,S., Schupback,R., Seaman,S., Severy,P., Spencer,B., Stange-Thomann,N., Stojanovic,N., Strauss,N., Subramanian,A., Talamas,J., Tesfaye,S., Theodore,J., Topham,K., Travers,M., Travis,N., Trigilio,J., Vassiliev,H., Viel,R., Vo,A., Wilson,B., Wu,X., Wyman,D., Ye,W.J., Young,G., Zainoun,J., Zembek,L., Zimmer,A. and Zody,M.

TITLE Direct Submission

JOURNAL Submitted (10-JUN-2002) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA

COMMENT On Jun 10, 2002 this sequence version replaced gi:19424573.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
-------------- Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
-------------- Project Information
Center project name: L24846
Center clone name: 455_M_3
-------------- Summary Statistics
Sequencing vector: Plasmid; n/a; 100% of reads
Chemistry: Dye-terminator Big Dye; 100% of reads
Assembly program: Phrap; version 0.960731
Consensus quality: 184146 bases at least Q40
Consensus quality: 187658 bases at least Q30
Consensus quality: 188723 bases at least Q20
Insert size: 183000; agarose-fp
Insert size: 189286; sum-of-contigs
Quality coverage: 6.1 in Q20 bases; agarose-fp
Quality coverage: 5.9 in Q20 bases; sum-of-contigs
--------------.
* NOTE: This is a 'working draft' sequence. It currently
* consists of 20 contigs. Gaps between the contigs
* are represented as runs of N. The order of the pieces
* is believed to be correct as given, however the sizes
* of the gaps between them are based on estimates that have
* provided by the submittor.
* This sequence will be replaced
* by the finished sequence as soon as it is available and
* the accession number will be preserved.

*	1	733: contig of 733 bp in length
*	734	833: gap of 100 bp
*	834	1739: contig of 906 bp in length
*	1740	1839: gap of 100 bp
*	1840	3536: contig of 1697 bp in length
*	3537	3636: gap of 100 bp
*	3637	5172: contig of 1536 bp in length
*	5173	5272: gap of 100 bp
*	5273	7064: contig of 1792 bp in length
*	7065	7164: gap of 100 bp
*	7165	9538: contig of 2374 bp in length
*	9539	9638: gap of 100 bp
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*	11845	11944: gap of 100 bp
*	11945	13280: contig of 1336 bp in length
*	13281	13380: gap of 100 bp
*	13381	16275: contig of 2895 bp in length
*	16276	16375: gap of 100 bp
*	16376	18626: contig of 2251 bp in length
*	18627	18726: gap of 100 bp
*	18727	23667: contig of 4941 bp in length
*	23668	23767: gap of 100 bp
*	23768	31948: contig of 8181 bp in length
*	31949	32048: gap of 100 bp
*	32049	39336: contig of 7288 bp in length
*	39337	39436: gap of 100 bp
*	39437	49369: contig of 9933 bp in length
*	49370	49469: gap of 100 bp
*	49470	61362: contig of 11893 bp in length
*	61363	61462: gap of 100 bp
*	61463	77912: contig of 16450 bp in length
*	77913	78012: gap of 100 bp
*	78013	92810: contig of 14798 bp in length
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*	92911	113012: contig of 20102 bp in length
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*	113113	137314: contig of 24202 bp in length
*	137315	137414: gap of 100 bp
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ORIGIN

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Qy        422 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 481
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Qy        482 TTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAA 541
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Qy        542 ACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCT 601
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Qy        602 TCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACAC 661
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Qy        662 AGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Search completed: November  7, 2004, 00:34:42
Job time : 3210 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 23:29:46 ; Search time 425 Seconds
(without alignments)
8732.566 Million cell updates/sec

Title: US-09-914-053A-6
Perfect score: 707
Sequence: 1 atgtcgatatggaccagtgg.....atccacggatcaatagataa 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4134886 seqs, 2624710521 residues

Total number of hits satisfying chosen parameters: 8269772

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_23Sep04:*
1: geneseqn1980s:*
2: geneseqn1990s:*
3: geneseqn2000s:*
4: geneseqn2001as:*
5: geneseqn2001bs:*
6: geneseqn2002as:*
7: geneseqn2002bs:*
8: geneseqn2003as:*
9: geneseqn2003bs:*
10: geneseqn2003cs:*
11: geneseqn2003ds:*
12: geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	706.2	99.9	707	3	AAA75011	Aaa75011 DNA encod
2	692	97.9	1184	4	AAF27991	Aaf27991 Human cal
3	690.4	97.7	1300	3	AAZ51632	Aaz51632 Human mem
4	564.2	79.8	2098	3	AAA26355	Aaa26355 Human sec
5	564.2	79.8	2098	8	ADA39669	Ada39669 Human sec
6	564.2	79.8	2098	10	ADA55858	Ada55858 Gene enco
7	564.2	79.8	2098	12	ADL71416	Adl71416 Novel hum
8	281	39.7	558	4	ABA09433	Aba09433 Human K c
9	135.4	19.2	1111	2	AAZ11913	Aaz11913 Human pot
10	135.4	19.2	1246	2	AAZ11912	Aaz11912 Human pot
11	134.4	19.0	774	3	AAA75009	Aaa75009 DNA encod
12	134.4	19.0	1144	4	AAK52128	Aak52128 Human pol
13	134.4	19.0	1251	4	ABA09214	Aba09214 Human Ca-
14	134.4	19.0	1251	4	AAK53112	Aak53112 Human pol
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16	134.4	19.0	1632	4	AAF27993	Aaf27993 Human cal
17	134	19.0	1106	2	AAT06477	Aat06477 Human cal
18	134	19.0	1277	6	ABL69681	Abl69681 Prostate
19	134	19.0	1277	10	ADD14749	Add14749 Human src
20	132.8	18.8	1237	4	AAF27992	Aaf27992 Human cal
21	131.2	18.6	1759	4	AAF27994	Aaf27994 Human cal
22	114.2	16.2	2238	2	AAT06476	Aat06476 Bovine ca
23	102.2	14.5	608	4	AAL02267	Aal02267 Human rep
c 24	80	11.3	110000	12	ADO34927_0	Ado34927 Human vol
25	75.8	10.7	1228	2	AAX82099	Aax82099 Human cal
26	74.8	10.6	188	3	AAC07442	Aac07442 Human sec
27	74.2	10.5	633	3	AAA75010	Aaa75010 DNA encod
28	74.2	10.5	1501	3	AAC75815	Aac75815 Human ORF
29	74.2	10.5	1608	3	AAZ22298	Aaz22298 Human pot
30	67	9.5	394	3	AAC03613	Aac03613 Human sec
31	60	8.5	60	6	ABN38341	Abn38341 Human spl
c 32	51.4	7.3	7045	4	ABA07292	Aba07292 Human pan
c 33	51.4	7.3	7045	4	AAK89937	Aak89937 Human dig
34	51.4	7.3	7045	4	AAL37429	Aal37429 Human mus
35	51.4	7.3	7045	8	ABX60417	Abx60417 cDNA enco
36	51.4	7.3	7045	12	ADJ31167	Adj31167 Human mus
c 37	49.2	7.0	413	12	ADO35047	Ado35047 Human KCh
38	47.2	6.7	285	2	AAT22677	Aat22677 Human gen
39	45.4	6.4	48000	4	AAF27996	Aaf27996 Human cal
40	44.8	6.3	2787	5	AAS77593	Aas77593 DNA encod
41	44.8	6.3	2787	5	AAS82312	Aas82312 DNA encod
42	44.8	6.3	2787	5	AAS77413	Aas77413 DNA encod
c 43	44.4	6.3	483	12	ADO35049	Ado35049 Human KCh
c 44	44.2	6.3	2000	8	ADA71938	Ada71938 Rice gene
45	43.2	6.1	898	6	ABQ25377	Abq25377 Oligonucl

ALIGNMENTS

RESULT 1
AAA75011
ID AAA75011 standard; DNA; 707 BP.
XX
AC AAA75011;
XX
DT 02-JAN-2001 (first entry)
XX
DE DNA encoding a human BK beta-4 polypeptide.
XX
KW Human; BK beta-2; beta subunit; Slo potassium channel; BK beta-3;
KW BK beta-4; ion flux; migraine; hearing; vision problem; seizure; stroke;
KW asthma; cell proliferation; hormone secretion; cancer; viral infection;
KW ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 1. .707
FT /*tag= a
FT /product= "BK beta-4"
FT /transl_except= (pos: 691. .692, aa: Gln)
XX
PN WO200050444-A1.
XX
PD 31-AUG-2000.
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PF 22-FEB-2000; 2000WO-US004441.
XX
PR 23-FEB-1999; 99US-0121224P.
PR 03-NOV-1999; 99US-0163367P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ, Wickenden A, Liu Y;
XX
DR WPI; 2000-533179/48.
DR P-PSDB; AAB08820.
XX
PT Isolated beta subunit polynucleotides and polypeptides of Slo potassium
PT channels are used to determine the effects of compounds on ion flux
PT through a potassium channel and in computer modelling systems.
XX
PS Claim 7; Page 79-80; 84pp; English.

XX
CC The present sequence encodes a human BK beta-4 polypeptide. The
CC polypeptide is a beta subunit of a Slo potassium channel. The
CC specification also describes BK beta-3 and BK beta-3 polypeptides. BK
CC beta subunits are auxiliary subunits or monomers of Slo potassium
CC channels. The polypeptides, when expressed in cells and cell membranes,
CC are used to determine the effects of compounds on ion flux through a
CC potassium channel. The compounds identified may be useful as therapeutic
CC agents e.g. modulators that target specific Slo channels are useful for
CC treating migraines, hearing and vision problems, seizures, stroke,
CC asthma, cell proliferation and hormone secretion. The computer generated
CC 3-dimensional structures of BK beta 2, BK beta 3 or BK beta 4 are used to
CC identify ligands that bind to the beta subunit. The characterized BK beta
CC subunits are used to determine how Slo potassium channels function in
CC different environments and how they respond to different activation
CC mechanisms. The polynucleotides are used to transfect cells in vivo and
CC in vitro to mitigate effects of absent, partial inactivation or abnormal
CC expression of the BK beta subunit gene e.g. to correct genetic defects,
CC cancer and viral infection
XX
SQ Sequence 707 BP; 205 A; 170 C; 153 G; 177 T; 0 U; 2 Other;

Query Match 99.9%; Score 706.2; DB 3; Length 707;
Best Local Similarity 100.0%; Pred. No. 5.1e-211;
Matches 707; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360

Qy        361 ACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        361 ACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCCACGGATCAATAGATAA 707
              ||||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGTACCTCTCCCTACTATGTGAGAGGATCCACGGATCAATAGATAA 707
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RESULT 2
AAF27991
ID AAF27991 standard; DNA; 1184 BP.
XX
AC AAF27991;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human calcium sensitive potassium channel beta2 subunit coding sequence.
XX
KW Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW irritable bowel syndrome; Alzheimer's disease; ds.
XX
OS Homo sapiens.
XX
PN WO200105828-A1.
XX
PD 25-JAN-2001.
XX
PF 18-JUL-2000; 2000WO-US019585.
XX
PR 20-JUL-1999; 99US-0144764P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Uebele V, Swanson R, Liu Y, Lagrutta A;
XX
DR WPI; 2001-159514/16.
DR P-PSDB; AAB35301.
XX
PT Novel human calcium sensitive potassium channel subunits for identifying
PT inhibitors and agonists of the potassium channel for use in treating
PT conditions such as asthma, hypertension, memory disorders, depression.
XX
PS Claim 3; Fig 1A; 89pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC and beta3d subunits. These can be used to identify inhibitors and
CC activators of the channels, which can be used in the treatment of
CC conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC incontinence, migraine and irritable bowel syndrome. The coding sequences
CC are found at human chromosome 3q23-ter. The present sequence is the beta2
CC subunit coding sequence
XX
SQ Sequence 1184 BP; 356 A; 260 C; 255 G; 313 T; 0 U; 0 Other;

Query Match 97.9%; Score 692; DB 4; Length 1184;
Best Local Similarity 99.3%; Pred. No. 1.9e-206;
Matches 703; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

```
Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              |||| ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        271 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 330

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        331 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 390

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 450

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 510

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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                    ||||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        511 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 570

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 630

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        631 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 690

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 750

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        751 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 810

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
                    ||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db        811 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 870

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
                    ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        871 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 930

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
                    |||||||||||||||||||||||||||| ||||||||||||||||
Db        931 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 978
```

RESULT 3
AAZ51632
ID AAZ51632 standard; cDNA; 1300 BP.
XX
AC AAZ51632;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human membrane channel protein-16 (MECHP-16) cDNA.
XX
KW Membrane channel protein-16; MECHP-16; diagnosis; treatment; lymphoma;
KW cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;
KW inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
KW diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
KW muscular disorder; myocarditis; Duchenne's muscular dystrophy; nootropic;
KW cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiant;
KW neurological disorder; Alzheimer's disease; Parkinson's disease; human;
KW Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;
KW anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
KW hypotensive; vasotropic; antiasthmatic; antiinflammatory; antidepressant;
KW anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 378. .1085
FT /*tag= a
FT /product= "MECHP-16"
FT /note= "Shows homology to human beta subunit of Ca+
FT activated K+ channel"
FT misc_binding 381. .425
FT /*tag= b
FT /bound_moiety= "Primer or Probe"
XX
PN WO200012711-A2.
XX
PD 09-MAR-2000.
XX
PF 02-SEP-1999; 99WO-US020468.
XX
PR 02-SEP-1998; 98US-0155226P.
PR 12-NOV-1998; 98US-00191283.
PR 09-DEC-1998; 98US-0155225P.
PR 26-JAN-1999; 99US-0155211P.
PR 10-FEB-1999; 99US-0155263P.
XX
PA (INCY-) INCYTE PHARM INC.
XX
PI Au-Young J, Bandman O, Tang YT, Reddy R, Hillman JL, Yue H;
PI Lal P, Corley NC, Guegler KJ, Gorgone G, Baughn MR, Azimzai Y;
XX
DR WPI; 2000-256643/22.
DR P-PSDB; AAY70466.
XX
PT Novel human membrane channel protein and polynucleotide useful for
PT diagnosing and treating cell proliferative, inflammatory, secretory,
PT osmoregulatory, muscular, cardiovascular and neurological disorders.
XX
PS Claim 9; Page 128-129; 140pp; English.
XX
CC The present sequence is a cDNA identified in Incyte clone 2069907 derived
CC from ISLTNOT01 cDNA library. It encodes human membrane channel protein-16
CC (MECHP-16), which is expressed in nervous tissues. Anti-MECHP antibodies
CC can be used as therapeutic antagonists and reagents for diagnosis and
CC monitoring diseases. MECHP cDNA can be used for diagnosis of MECHP-
CC related diseases and gene mapping. MECHP can be used for treatment of
CC cell proliferative disorders such as bursitis and atherosclerosis,
CC cancers like lymphoma and sarcoma, inflammatory disorders like AIDS and
CC Addison's disease, transport/secretory disorders like cystic fibrosis and
CC diabetes mellitus, osmoregulatory disorders like diarrhoea and renal
CC failure, muscular disorders like myocarditis and Duchenne's muscular
CC dystrophy, cardiovascular disorders like hypertension and vasculitis,
CC congenital lung anomalies like bronchitis and asthma and neurological
CC disorders like Alzheimer's disease, Parkinson's disease and Huntington's
CC disease
XX
SQ Sequence 1300 BP; 381 A; 288 C; 279 G; 352 T; 0 U; 0 Other;

Query Match 97.7%; Score 690.4; DB 3; Length 1300;
Best Local Similarity 99.2%; Pred. No. 6.5e-206;
Matches 702; Conservative 2; Mismatches 3; Indels 1; Gaps 1;

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Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
                  ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        378 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 437

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        438 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 497

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        498 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 557

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 617

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYGTCTCCTTCAGC 300
                  ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        618 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 677

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
                  ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||
Db        678 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCCCCAGGTGTACGTTAACCTG 737

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        738 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 797

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
                  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        798 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 857
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Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        858 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 917

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              |||||||||||||||||||||||:|||||||||||||||||||||||||||||||||||
Db        918 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 977

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        978 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 1037

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||||||||||||||| ||||||||||||||||
Db       1038 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 1085
```

RESULT 4
AAA26355
ID AAA26355 standard; cDNA; 2098 BP.
XX
AC AAA26355;
XX
DT 29-JUN-2000 (first entry)
XX
DE Human secreted protein gene 10 SEQ ID NO:20.
XX
KW Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW immune disease; inflammation; blood disorder; tumour; ss.
XX
OS Homo sapiens.
XX
PN WO200006698-A1.
XX
PD 10-FEB-2000.
XX
PF 29-JUL-1999; 99WO-US017130.
XX
PR 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX
DR WPI; 2000-195282/17.
DR P-PSDB; AAY91460.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 1; Page 378-379; 634pp; English.
XX
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Query Match 79.8%; Score 564.2; DB 3; Length 2098;
Best Local Similarity 99.5%; Pred. No. 3.9e-166;
Matches 574; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

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Qy        132 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 68

Qy        192 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 128

Qy        252 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGCTGTGGTCCAGA 311
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        129 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGA 188

Qy        312 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 248

Qy        372 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 308

Qy        432 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 368

Qy        492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 428

Qy        552 TGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 611
              ||||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 488

Qy        612 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 548

Qy        672 CCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||||| ||||||||||||||||
Db        549 CCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 585
```

RESULT 5
ADA39669
ID ADA39669 standard; cDNA; 2098 BP.
XX
AC ADA39669;
XX
DT 20-NOV-2003 (first entry)
XX
DE Human secreted protein encoding cDNA.
XX
KW Human; secreted protein; cancer; hyperproliferative disorder;

KW rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW anaemia; allergic reaction; asthma; cardiovascular disorder;
KW wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW vulnerary; cardiant; gene therapy; ss.
XX
OS Homo sapiens.
XX
PN WO2002102993-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008123.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-175238/17.
XX
PT New human secreted proteins and nucleic acid molecules, useful for
PT preparing a diagnostic or pharmaceutical composition for diagnosing,
PT preventing or treating cancer or other hyperproliferative disorder,
PT asthma, allergies or AIDS.
XX
PS Claim 9; SEQ ID NO 51; 3205pp; English.
XX
CC The invention relates to novel genes ADA39629-ADA40565 and proteins
CC ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC treating or ameliorating medical conditions e.g. by protein or gene
CC therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC fragments, and agonists or antagonists that bind to the polypeptide are
CC useful for preparing a diagnostic or pharmaceutical composition for
CC diagnosing or treating cancer or other hyperproliferative disorder. The
CC polypeptides and nucleic acid molecules are also useful for detecting,
CC preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC or other hyperproliferative disorders including neoplasms, autoimmune
CC disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC thrombocytopenia), allergic reactions including asthma or eczema,
CC inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC fungal or viral infections including HIV/AIDS), or wound healing and
CC disorders of epithelial cell proliferation. The nucleic acids are also
CC useful for chromosome identification, radiation hybrid mapping or long-
CC range restriction mapping, as molecular weight markers, or as
CC hybridization or diagnostic probes. The polypeptides and antibodies are
CC useful for providing immunological probes for differential identification
CC of the tissues immunohistochemistry assays. Note: The sequence data for
CC this patent did not form part of the printed specification, but was
CC obtained in electronic format directly from WIPO at
CC ftp.wipo.int/pub/published_pct_sequences.
XX
SQ Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Query Match 79.8%; Score 564.2; DB 8; Length 2098;
Best Local Similarity 99.5%; Pred. No. 3.9e-166;
Matches 574; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```
Qy        132 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 68

Qy        192 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 128

Qy        252 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGCTGTGGTCCAGA 311
              ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db        129 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGA 188

Qy        312 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 248

Qy        372 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 308

Qy        432 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 368

Qy        492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 428

Qy        552 TGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 611
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 488

Qy        612 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 548

Qy        672 CCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||||| ||||||||||||||||
Db        549 CCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 585
```

RESULT 6
ADA55858
ID ADA55858 standard; DNA; 2098 BP.
XX
AC ADA55858;
XX
DT 20-NOV-2003 (first entry)
XX
DE Gene encoding human secreted protein #37.
XX
KW immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW cytostatic; cerebroprotective; neuroprotective; nootropic;
KW cardiovascular; antiarteriosclerotic; gene therapy;
KW human secreted protein; immune disorder; inflammation;
KW respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW triple helix formation; antisense gene therapy; forensic biology; ds;
KW gene.
XX
OS Homo sapiens.
XX
PN WO2002102994-A2.
XX
PD 27-DEC-2002.
XX
PF 19-MAR-2002; 2002WO-US008278.
XX
PR 21-MAR-2001; 2001US-0277340P.
PR 19-JUL-2001; 2001US-0306171P.
PR 13-NOV-2001; 2001US-0331287P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Rosen CA, Ruben SM;
XX
DR WPI; 2003-167512/16.
DR P-PSDB; ADA56755.

```
XX
PT   New human secreted polypeptides and polynucleotides, useful for
PT   diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT   conditions, respiratory disorders, cancers, CNS disorders, or
PT   neurodegenerative disorders.
XX
PS   Claim 21; SEQ ID NO 47; 1754pp; English.
XX
CC   The invention relates to 592 new human secreted polypeptides useful for
CC   diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC   conditions, respiratory disorders, cancers, CNS disorders, or
CC   neurodegenerative disorders, or polypeptides comprising an amino acid
CC   sequence at least 95% identical to the new sequences. The polypeptides,
CC   antibodies or antibody fragments that bind to the polypeptides, nucleic
CC   acids encoding the polypeptides, agonists or antagonists that binds to
CC   the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC   compositions for diagnosing, treating or preventing an e.g. immune
CC   disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC   nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC   allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC   (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC   disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC   cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC   polynucleotides are useful for chromosome identification, chromosome
CC   mapping, for controlling gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy, for identifying individuals
CC   from minute biological samples, in forensic biology, and as hybridization
CC   probes. The polypeptides are useful for as molecular weight markers on
CC   sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   gels, to raise antibodies, for testing biological activities, and for
CC   treating or preventing neural disorders, immune system disorders,
CC   muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC   renal, proliferative and/or cancerous diseases. This sequence corresponds
CC   to a gene encoding one of the polypeptide of the invention. Note: The
CC   sequence data for this patent did form part of the printed specification,
CC   but was obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

  Query Match             79.8%;  Score 564.2;  DB 10;  Length 2098;
  Best Local Similarity   99.5%;  Pred. No. 3.9e-166;
  Matches  574;  Conservative    2;  Mismatches    0;  Indels    1;  Gaps    1;

Qy        132 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 191
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          9 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 68

Qy        192 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 251
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         69 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 128

Qy        252 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGCTGTGGTCCAGA 311
              ||||||||||||||||||||||||||||||||||:||||||||||||||||||||||||
Db        129 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGA 188

Qy        312 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 371
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        189 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 248

Qy        372 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 431
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        249 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 308

Qy        432 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 491
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        309 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 368

Qy        492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        369 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 428

Qy        552 TGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 611
              ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db        429 TGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 488

Qy        612 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 671
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        489 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 548

Qy        672 CCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||||| ||||||||||||||||
Db        549 CCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 585


RESULT 7
ADL71416
ID   ADL71416 standard; cDNA; 2098 BP.
XX
AC   ADL71416;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Novel human secreted protein cDNA seqid 20.
XX
KW   antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; antilipaemic; CNS; gynaecological; antiarthritic;
KW   antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
KW   immunosuppressive; antiallergic; cardiovascular; respiratory;
KW   dermatological; antimicrobial; gastrointestinal; gene therapy;
KW   neurodegenerative disease; behavioral disorder; inflammatory condition;
KW   hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW   Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW   arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW   Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW   leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW   respiratory disorder; pulmonary disorder; connective tissue disorder;
KW   skin disorder; CNS disorder; congenital disorder; infectious disorder;
KW   gastrointestinal disorder; human; secreted protein; gene; ss.
XX
OS   Homo sapiens.
XX
PN   US2004034196-A1.
XX
PD   19-FEB-2004.
XX
PF   27-JAN-2003; 2003US-00351334.
XX
PR   30-JUL-1998;   98US-0094657P.
PR   05-AUG-1998;   98US-0095486P.
PR   06-AUG-1998;   98US-0095454P.
PR   06-AUG-1998;   98US-0095455P.
PR   12-AUG-1998;   98US-0096319P.
PR   29-JUL-1999;   99WO-US017130.
PR   24-JAN-2000; 2000US-00489847.
PR   25-JAN-2002; 2002US-0350898P.
XX
PA   (KOMA/) KOMATSOULIS G A.
PA   (ROSE/) ROSEN C A.
PA   (RUBE/) RUBEN S M.
PA   (DUAN/) DUAN D R.
PA   (MOOR/) MOORE P A.
PA   (SHIY/) SHI Y.
PA   (LAFL/) LAFLEUR D W.
PA   (WEIY/) WEI Y.
XX
PI   Komatsoulis GA,  Rosen CA,  Ruben SM,  Duan DR,  Moore PA,  Shi Y;
PI   Lafleur DW,  Wei Y;
XX
DR   WPI; 2004-180094/17.
DR   P-PSDB; ADL71532.
XX
PT   New human secreted nucleic acid, useful for diagnosing and treating
PT   neurodegenerative, inflammatory, hyperproliferative, metabolic,
PT   reproductive, cardiovascular, respiratory or immunological disorders or
```

PT diseases.
XX
PS Claim 1; SEQ ID NO 20; 234pp; English.
XX
CC The invention describes an isolated human nucleic acid molecule (I)
CC comprising a polynucleotide having a nucleotide sequence at least 95%
CC identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
CC the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
CC to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
CC epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
CC sequence included in ATCC Deposit No: Z, which is hybridisable to SEQ ID
CC NO: X, having a biological activity. The nucleic acids and polypeptides,
CC pharmaceutical formulations and kits are useful in diagnosing and
CC treating neurodegenerative diseases states, behavioral disorders,
CC inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
CC disease, Parkinson's diseases or Huntington's diseases), metabolic
CC disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
CC disorders, immunological disorders (e.g. arthritis, asthma or AIDS),
CC endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
CC or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
CC cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
CC conditions afflicting connective tissue, skin disorders, CNS disorders,
CC congenital disorders, infectious disorders and gastrointestinal
CC disorders. This sequence encodes a novel human secreted protein of the
CC invention. Note: This sequence does not appear in the printed
CC specification but is available in electronic format from the US patent
CC office at ftp.seqdata.uspto.gov/seqdata.html?DocID=20040034196.
XX
SQ Sequence 2098 BP; 645 A; 366 C; 368 G; 719 T; 0 U; 0 Other;

Query Match 79.8%; Score 564.2; DB 12; Length 2098;
Best Local Similarity 99.5%; Pred. No. 3.9e-166;
Matches 574; Conservative 2; Mismatches 0; Indels 1; Gaps 1;

```
Qy      132 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 191
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        9 GGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCT 68

Qy      192 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 251
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       69 GCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATG 128

Qy      252 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGCTGTGGTCCAGA 311
            ||||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||
Db      129 CACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGA 188

Qy      312 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 371
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      189 CTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGG 248

Qy      372 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 431
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      249 GGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTA 308

Qy      432 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 491
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      309 TATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGA 368

Qy      492 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 551
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      369 AAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAG 428

Qy      552 TGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 611
            ||||||||||||:||||||||||||||||||||||||||||||||||||||||||||||
Db      429 TGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAAC 488

Qy      612 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 671
            ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db      489 CTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTC 548

Qy      672 CCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
            |||||||||||||||||||| |||||||||||||||
Db      549 CCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 585
```

RESULT 8
ABA09433
ID ABA09433 standard; cDNA; 558 BP.
XX
AC ABA09433;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human K channel subunit homologue-encoding cDNA, SEQ ID NO:1209.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer; ss.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR P-PSDB; ABB12189.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 1; Page 945; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,

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CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention
XX
SQ   Sequence 558 BP; 165 A; 128 C; 144 G; 121 T; 0 U; 0 Other;

  Query Match             39.7%;  Score 281;  DB 4;  Length 558;
  Best Local Similarity   97.6%;  Pred. No. 2e-77;
  Matches  284;  Conservative    1;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        268 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAGAGAAAT 327

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              |||||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        328 ATTTACCAGAGAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 387

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        388 AAGGCAGGAGAGGACCGAGCTATTCTACTGGGACTGGCTATGATGGTGTGCTCCATCATG 447

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||| |||||||||||||||||||||||||||||||||||||||||||||||||   |
Db        448 ATGTAATTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCCGA 507

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGC 291
              ||||||||||||||||||||||||||||||||||||||||||||||:|||
Db        508 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGC 558


RESULT 9
AAZ11913
ID   AAZ11913 standard; cDNA; 1111 BP.
XX
AC   AAZ11913;
XX
DT   30-NOV-1999  (first entry)
XX
DE   Human potassium channel K+Hnov44 cDNA (splice variant 2).
XX
KW   Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW   cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   CDS             297. .959
FT                   /*tag=  a
FT                   /product= "Human K+Hnov44 potassium channel"
XX
PN   WO9943696-A1.
XX
PD   02-SEP-1999.
XX
PF   22-FEB-1999;   99WO-US003826.
XX
PR   25-FEB-1998;   98US-0076687P.
PR   07-AUG-1998;   98US-0095836P.
PR   19-JAN-1999;   99US-0116448P.
XX
PA   (AXYS-) AXYS PHARM INC.
XX
PI   Miller AP,  Curran ME,  Hu P,  Rutter M,  Wang J;
XX
DR   WPI; 1999-527591/44.
DR   P-PSDB; AAY34131.
XX
PT   New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
PT   useful for the diagnosis and treatment of episodic ataxia with myokymia,
PT   cardiac arrhythmia, epilepsy and Bartter's syndrome.
XX
PS   Claim 4; Page 90-91; 112pp; English.
XX
CC   This sequence represents splice variant 2 of a human potassium channel
CC   K+Hnov44 cDNA. Alternative splicing does not affect the amino acid
CC   sequence of the protein. K+Hnov proteins have a high degree of homology
CC   to known potassium channels and may be alpha subunits, which form the
CC   functional channel, or accessory subunits that act to modulate the
CC   channel activity. K+Hnov44 is a potassium channel beta subunit. The
CC   gene's chromosomal location is 22p13, determined via PCR chromosomal
CC   localisation using primers AAZ11934 and AAZ11936. K+Hnov cDNAs were
CC   isolated by extension of expressed sequence tags (ESTs) which were
CC   related but not identical to known human potassium channels. Potential
CC   polymorphisms detected as sequence variants between multiple independent
CC   clones. Potassium channels have critical roles in various cell types and
CC   biochemical pathways. Defective potassium channels are known to cause
CC   four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
CC   (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
CC   channels are critical components of virtually all cells, it is likely
CC   that abnormal potassium channels are also implicated in certain renal,
CC   cardiovascular and central nervous system (CNS) disorders. Nucleotides
CC   encoding K+Hnov proteins may be used for identifying homologous or
CC   related proteins and the DNA sequences encoding them. They may be used to
CC   produce compositions that modulate the expression and function of the
CC   K+Hnov protein and in studying the biochemical pathways associated with
CC   it. They may also be used for the recombinant production of K+Hnov
CC   protein in fermentation cultures. Additionally, such nucleotides may be
CC   used in gene therapy protocols for the treatment of diseases associated
CC   with abnormal potassium channels
XX
SQ   Sequence 1111 BP; 347 A; 237 C; 263 G; 264 T; 0 U; 0 Other;

  Query Match             19.2%;  Score 135.4;  DB 2;  Length 1111;
  Best Local Similarity   54.6%;  Pred. No. 1.7e-31;
  Matches  312;  Conservative    2;  Mismatches  248;  Indels    9;  Gaps    2;

Qy        124 GCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATG 183
              || |||||||||||||||   | |||||  | || |||||||  | |||  || | |||
Db        276 GCTGGAGAGGACCGAGCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATG 335

Qy        184 TATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAG 243
              |   ||  |||| ||||  ||  | ||       | |  ||||  |||  |   ||  |||||
Db        336 TTCTTCTTGCTCGGAACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAA 395

Qy        244 TCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACAT---TTAAYTGCTCCTTCAGC 300
              ||    |||||    |  |  |    |||| |||     |   |  |:||  |||||| |
Db        396 TCGACCTGCACTGCCATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACC 455

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              ||||||    |||||       |     ||||||| || || |||||||  || |||||
Db        456 TGTGGTGTGCACTGCCACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTC 515

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |    | | ||  | ||     |||||  |  | |  |||||| |   |  | || ||||
Db        516 AGCCATCCAGGTCAGAAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCC 575

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              |||||||  || | ||||||||      || ||    | || |   |   |   |
Db        576 AAGTGCTTTTACACACCTAAGTGCCACCAAGATAGAAATGATTTGCTCAACAGTGCTCTG 635

Qy        481 GTTGTCATGGAAAACTT------CAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCA 534
              |   | |  |||  |||      ||  ||        | ||| || |||| |    |||
Db        636 GACATAAAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCA 695
```

```
Qy        535 GAAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCAT 594
              |  |  |     |  ||| || || | :|||  ||       |  |   | |||||
Db        696 GCCAGCCAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCAC 755

Qy        595 TCACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAA 654
              |  | || |||||  |    |   ||  || ||||     ||||||| ||||||||  |
Db        756 TGTTTATTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGA 815

Qy        655 CTTACACAGTACCTCTCCCTACTATGTGAGA 685
              | |||||  |||| ||| |||| ||||| |
Db        816 TTAACACAACACCTGTCCTTACTGTGTGAAA 846
```

RESULT 10
AAZ11912
ID AAZ11912 standard; cDNA; 1246 BP.
XX
AC AAZ11912;
XX
DT 30-NOV-1999 (first entry)
XX
DE Human potassium channel K+Hnov44 cDNA (splice variant 1).
XX
KW Potassium channel; ataxia; arrhythmia; epilepsy; Bartter's syndrome;
KW cardiovascular disorder; CNS disorder; renal disorder; ds.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 432. .1094
FT /*tag= a
FT /product= "Human K+Hnov44 potassium channel"
XX
PN WO9943696-A1.
XX
PD 02-SEP-1999.
XX
PF 22-FEB-1999; 99WO-US003826.
XX
PR 25-FEB-1998; 98US-0076687P.
PR 07-AUG-1998; 98US-0095836P.
PR 19-JAN-1999; 99US-0116448P.
XX
PA (AXYS-) AXYS PHARM INC.
XX
PI Miller AP, Curran ME, Hu P, Rutter M, Wang J;
XX
DR WPI; 1999-527591/44.
DR P-PSDB; AAY34131.
XX
PT New nucleic acids encoding mammalian K+Hnov potassium channel proteins,
PT useful for the diagnosis and treatment of episodic ataxia with myokymia,
PT cardiac arrhythmia, epilepsy and Bartter's syndrome.
XX
PS Claim 4; Page 89-90; 112pp; English.
XX
CC This sequence represents splice variant 1 of a human potassium channel
CC K+Hnov44 cDNA. Alternative splicing does not affect the amino acid
CC sequence of the protein. K+Hnov proteins have a high degree of homology
CC to known potassium channels and may be alpha subunits, which form the
CC functional channel, or accessory subunits that act to modulate the
CC channel activity. K+Hnov44 is a potassium channel beta subunit. The
CC gene's chromosomal location is 22p13, determined via PCR chromosomal
CC localisation using primers AAZ11934 and AAZ11936. K+Hnov cDNAs were
CC isolated by extension of expressed sequence tags (ESTs) which were
CC related but not identical to known human potassium channels. Potential
CC polymorphisms detected as sequence variants between multiple independent
CC clones. Potassium channels have critical roles in various cell types and
CC biochemical pathways. Defective potassium channels are known to cause
CC four human diseases: episodic ataxia with myokymia; cardiac arrhythmia
CC (long QT syndrome); epilepsy; and Bartter's syndrome. As potassium
CC channels are critical components of virtually all cells, it is likely
CC that abnormal potassium channels are also implicated in certain renal,
CC cardiovascular and central nervous system (CNS) disorders. Nucleotides
CC encoding K+Hnov proteins may be used for identifying homologous or
CC related proteins and the DNA sequences encoding them. They may be used to
CC produce compositions that modulate the expression and function of the
CC K+Hnov protein and in studying the biochemical pathways associated with
CC it. They may also be used for the recombinant production of K+Hnov
CC protein in fermentation cultures. Additionally, such nucleotides may be
CC used in gene therapy protocols for the treatment of diseases associated
CC with abnormal potassium channels
XX
SQ Sequence 1246 BP; 345 A; 299 C; 302 G; 300 T; 0 U; 0 Other;

Query Match 19.2%; Score 135.4; DB 2; Length 1246;
Best Local Similarity 54.6%; Pred. No. 1.8e-31;
Matches 312; Conservative 2; Mismatches 248; Indels 9; Gaps 2;

```
Qy        124 GCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATG 183
              || |||||||||||||  |  | |||||  | || |||||||  | |||  || | |||
Db        411 GCTGGAGAGGACCGAGCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATG 470

Qy o      184 TATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAG 243
              |  ||  |||| ||||  ||  | ||     | |  ||||  |||  |   ||  |||||
Db        471 TTCTTCTTGCTCGGAACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAA 530

Qy        244 TCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACAT---TTAAYTGCTCCTTCAGC 300
              ||    ||||      |  |    |||| |||    |    |  |:||  |||||| |
Db        531 TCGACCTGCACTGCCATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACC 590

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              ||||||    |||||       |       ||||||| || || |||||||  || |||||
Db        591 TGTGGTGTGCACTGCCACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTC 650

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |  | |  ||  | ||      |||||  |  | |  ||||||  |  |  | || ||||
Db        651 AGCCATCCAGGTCAGAAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCC 710

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              |||||||  || | ||||||  ||      ||  ||    | ||  |  |  |  |
Db        711 AAGTGCTTTTACACACCTAAGTGCCACCAAGATAGAAATGATTTGCTCAACAGTGCTCTG 770

Qy        481 GTTGTCATGGAAAACTT------CAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCA 534
              |   | |  |||  |||       ||  ||      | ||| || ||||  |     |||
Db        771 GACATAAAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCA 830

Qy        535 GAAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCAT 594
              |  |  |     |  ||| || || | :|||  ||       |  |   | |||||
Db        831 GCCAGCCAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCAC 890

Qy        595 TCACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAA 654
              |  | || |||||  |    |   ||  || ||||     ||||||| ||||||||  |
Db        891 TGTTTATTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGA 950

Qy        655 CTTACACAGTACCTCTCCCTACTATGTGAGA 685
              | |||||  |||| ||| |||| ||||| |
Db        951 TTAACACAACACCTGTCCTTACTGTGTGAAA 981
```

RESULT 11
AAA75009
ID AAA75009 standard; DNA; 774 BP.
XX
AC AAA75009;
XX
DT 02-JAN-2001 (first entry)
XX
DE DNA encoding a human BK beta-2 polypeptide.
XX
KW Human; BK beta-2; beta subunit; Slo potassium channel; BK beta-3;
KW BK beta-4; ion flux; migraine; hearing; vision problem; seizure; stroke;
KW asthma; cell proliferation; hormone secretion; cancer; viral infection;
KW ss.
XX
OS Homo sapiens.

```
XX
FH   Key             Location/Qualifiers
FT   CDS             1. .774
FT                   /*tag= a
FT                   /product= "BK beta-2"
XX
PN   WO200050444-A1.
XX
PD   31-AUG-2000.
XX
PF   22-FEB-2000; 2000WO-US004441.
XX
PR   23-FEB-1999;   99US-0121224P.
PR   03-NOV-1999;   99US-0163367P.
XX
PA   (ICAG-) ICAGEN INC.
XX
PI   Jegla TJ,  Wickenden A,  Liu Y;
XX
DR   WPI; 2000-533179/48.
DR   P-PSDB; AAB08818.
XX
PT   Isolated beta subunit polynucleotides and polypeptides of Slo potassium
PT   channels are used to determine the effects of compounds on ion flux
PT   through a potassium channel and in computer modelling systems.
XX
PS   Claim 7; Page 79; 84pp; English.
XX
CC   The present sequence encodes a human BK beta-2 polypeptide. The
CC   polypeptide is a beta subunit of a Slo potassium channel. The
CC   specification also describes BK beta-3 and BK beta-4 polypeptides. BK
CC   beta subunits are auxiliary subunits or monomers of Slo potassium
CC   channels. The polypeptides, when expressed in cells and cell membranes,
CC   are used to determine the effects of compounds on ion flux through a
CC   potassium channel. The compounds identified may be useful as therapeutic
CC   agents e.g. modulators that target specific Slo channels are useful for
CC   treating migraines, hearing and vision problems, seizures, stroke,
CC   asthma, cell proliferation and hormone secretion. The computer generated
CC   3-dimensional structures of BK beta 2, BK beta 3 or BK beta 4 are used to
CC   identify ligands that bind to the beta subunit. The characterized BK beta
CC   subunits are used to determine how Slo potassium channels function in
CC   different environments and how they respond to different activation
CC   mechanisms. The polynucleotides are used to transfect cells in vivo and
CC   in vitro to mitigate effects of absent, partial inactivation or abnormal
CC   expression of the BK beta subunit gene e.g. to correct genetic defects,
CC   cancer and viral infection
XX
SQ   Sequence 774 BP; 223 A; 177 C; 179 G; 195 T; 0 U; 0 Other;

  Query Match             19.0%;  Score 134.4;  DB 3;  Length 774;
  Best Local Similarity   54.6%;  Pred. No. 2.8e-31;
  Matches  311;  Conservative    2;  Mismatches  248;  Indels    9;  Gaps    2;

Qy        125 CAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGT 184
              | ||||||||||||||||  |  | |||||  | || |||||||  | |||  || | ||||
Db         92 CTGGAGAGGACCGAGCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGT 151

Qy        185 ATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGT 244
                ||  |||| ||||  ||  | ||      | |  ||||  |||| |   ||  ||||| |
Db        152 TCTTCTTGCTCGGAACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAAT 211

Qy        245 CTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACAT---TTAAYTGCTCCTTCAGCT 301
              |   |||||      |  |  |    |||| |||    |   |  |:||  |||||| ||
Db        212 CGACCTGCACTGCCATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCT 271

Qy        302 GTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGA 361
              |||||    |||||      |      ||||||| || || |||||||  || |||||
Db        272 GTGGTGTGCACTGCCACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCA 331

Qy        362 CTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGA 421
              | | ||  | ||    |||||  |  | |  ||||||  |   |  | || ||||  |
Db        332 GCCATCCAGGTCAGAAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCA 391

Qy        422 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 481
              ||||||  || | ||||||| ||      || ||    | || | |   |   |     |
Db        392 AGTGCTTTTACACACCTAAGTGCCACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGG 451

Qy        482 TTGTCATGGAAAACTT------CAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAG 535
                | |  |||  |||       ||  ||       | ||| || ||||  |     ||||
Db        452 ACATAAAAGAATTCTTCGATCACAAAAATGGAACCCCCTTTTCATGCTTCTACAGTCCAG 511

Qy        536 AAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATT 595
                |  |      |  ||| || || | :|||   ||       |  |   | |||||  |
Db        512 CCAGCCAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACT 571

Qy        596 CACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAAC 655
              | || |||||  |    |  ||  || ||||      |||||||  ||||||||  |
Db        572 GTTTATTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGAT 631

Qy        656 TTACACAGTACCTCTCCCTACTATGTGAGA 685
              | |||||  |||| ||| |||| ||||| |
Db        632 TAACACAACACCTGTCCTTACTGTGTGAAA 661


RESULT 12
AAK52128
ID   AAK52128 standard; cDNA; 1144 BP.
XX
AC   AAK52128;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human polynucleotide SEQ ID NO 673.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   P-PSDB; AAM78995.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 1; Page 2356-2357; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
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CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 1144 BP; 289 A; 296 C; 291 G; 268 T; 0 U; 0 Other;

  Query Match             19.0%;  Score 134.4;  DB 4;  Length 1144;
  Best Local Similarity   54.6%;  Pred. No. 3.5e-31;
  Matches  311;  Conservative    2;  Mismatches  248;  Indels    9;  Gaps    2;

Qy        125 CAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGT 184
              | ||||||||||||||   |  | |||||  | || |||||||  | |||  || | ||||
Db        465 CTGGAGAGGACCGAGCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGT 524

Qy        185 ATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGT 244
              ||  |||| |||| ||  | ||     | |  ||||  ||| |   ||  ||||| |
Db        525 TCTTCTTGCTCGGAACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAAT 584

Qy        245 CTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACAT---TTAAYTGCTCCTTCAGCT 301
              |    |||||      |  |  |    |||| |||     |   |  |:||  |||||| ||
Db        585 CGACCTGCACTGCCATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCT 644

Qy        302 GTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGA 361
              |||||    ||||        |        ||||||| || || |||||||  || ||||| |
Db        645 GTGGTGTGCACTGCCACGGTCAGGGGAAGTACCCATGTCTTCAGGTGTTTGTGAACCTCA 704

Qy        362 CTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGA 421
              | | ||  | ||    |||||  |  | |  ||||||  |  |  | ||  ||||  |
Db        705 GCCATCCAGGTCAGAAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCA 764

Qy        422 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 481
              ||||||  ||  | |||||| ||     || ||    | || |   |   |   |     |
Db        765 AGTGCTTTTACACACCTAAGTGCCACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGG 824

Qy        482 TTGTCATGGAAAACTT------CAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAG 535
              | |  |||  |||       ||  ||       | ||| || ||||  |     ||||
Db        825 ACATAAAAGAATTCTTCGATCACAAAAATGGAACTCCCTTTTCATGCTTCTACAGTCCAG 884

Qy        536 AAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATT 595
              |  |      |   ||| || || | :|||   ||        |  |   | ||||| |
Db        885 CCAGCCAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACT 944

Qy        596 CACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAAC 655
              | || |||||  |   |  ||  || ||||      |||||||  ||||||||  |
Db        945 GTTTATTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGAT 1004

Qy        656 TTACACAGTACCTCTCCCTACTATGTGAGA 685
              | |||||  ||||  |||  ||||  ||||| |
Db       1005 TAACACAACACCTGTCCTTACTGTGTGAAA 1034


RESULT 13
ABA09214
ID   ABA09214 standard; cDNA; 1251 BP.
XX
AC   ABA09214;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human Ca-activated K channel homologue-encoding cDNA, SEQ ID NO:990.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer; ss.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US003800.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   P-PSDB; ABB11970.
XX
PT   Human proteins and DNA encoding sequences useful for preventing, treating
PT   or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT   and cancer.
XX
PS   Claim 1; Page 843-844; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a cDNA encoding a
CC   novel human polypeptide of the invention
XX
SQ   Sequence 1251 BP; 331 A; 304 C; 310 G; 306 T; 0 U; 0 Other;

  Query Match             19.0%;  Score 134.4;  DB 4;  Length 1251;
  Best Local Similarity   54.6%;  Pred. No. 3.7e-31;
  Matches  311;  Conservative    2;  Mismatches  248;  Indels    9;  Gaps    2;
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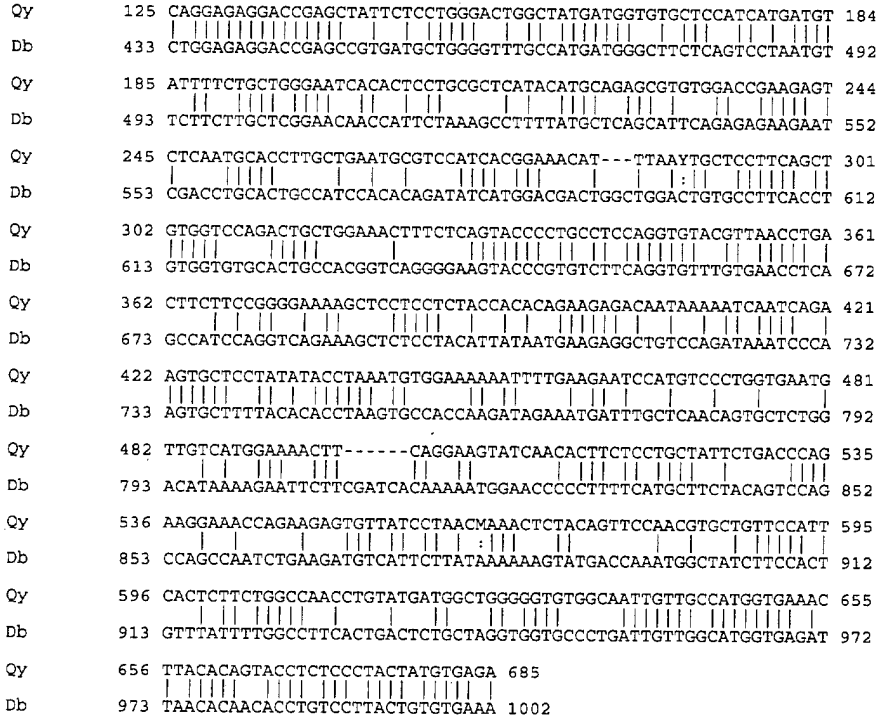
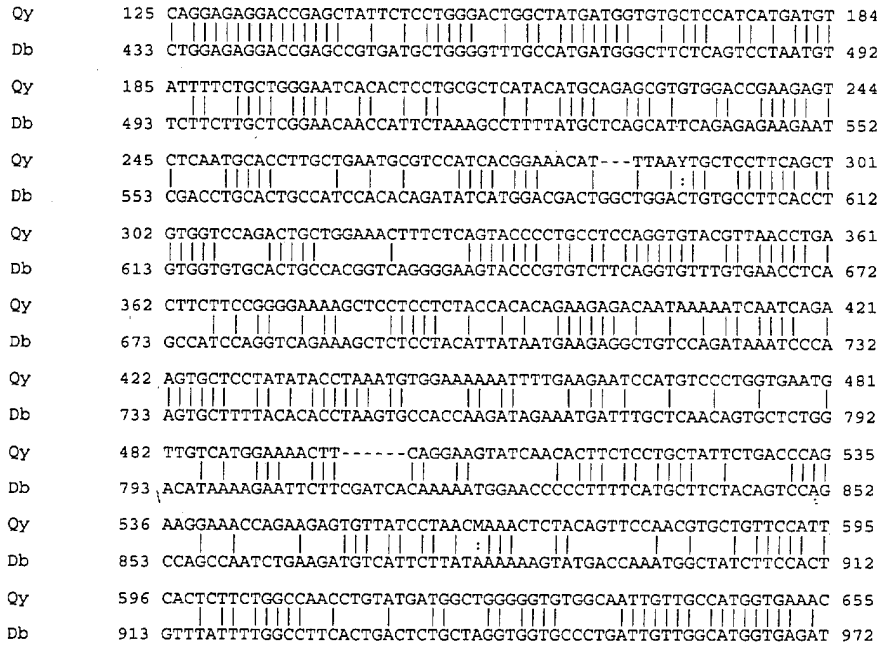


RESULT 14
AAK53112
ID AAK53112 standard; cDNA; 1251 BP.
XX
AC AAK53112;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human polynucleotide SEQ ID NO 2641.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation; ss.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;
XX
DR WPI; 2001-476283/51.
DR P-PSDB; AAM79979.
XX
PT Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT in diagnosis and gene therapy.
XX
PS Claim 1; Page 4899-4900; 6221pp; English.
XX
CC The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC cytokine, cell proliferation or cell differentiation or which may induce
CC production of other cytokines in other cell populations. The
CC polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC peptide therapy. The polypeptides have various cytokine-like activities,
CC e.g. stem cell growth factor activity, haematopoiesis regulating
CC activity, tissue growth factor activity, immunomodulatory activity and
CC activin/inhibin activity and may be useful in the diagnosis and/or
CC treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC sequence listing were missing at the time of publication
XX
SQ Sequence 1251 BP; 331 A; 304 C; 310 G; 306 T; 0 U; 0 Other;

Query Match 19.0%; Score 134.4; DB 4; Length 1251;
Best Local Similarity 54.6%; Pred. No. 3.7e-31;
Matches 311; Conservative 2; Mismatches 248; Indels 9; Gaps 2;



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Db        973 TAACACAACACCTGTCCTTACTGTGTGAAA 1002


RESULT 15
AAF27995
ID   AAF27995 standard; DNA; 1296 BP.
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AC   AAF27995;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human calcium sensitive potassium channel beta3d subunit coding sequence.
XX
KW   Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW   beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW   chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW   irritable bowel syndrome; Alzheimer's disease; ds.
XX
OS   Homo sapiens.
XX
PN   WO200105828-A1.
XX
PD   25-JAN-2001.
XX
PF   18-JUL-2000; 2000WO-US019585.
XX
PR   20-JUL-1999;   99US-0144764P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Uebele V,  Swanson R,  Liu Y,  Lagrutta A;
XX
DR   WPI; 2001-159514/16.
DR   P-PSDB; AAB35305.
XX
PT   Novel human calcium sensitive potassium channel subunits for identifying
PT   inhibitors and agonists of the potassium channel for use in treating
PT   conditions such as asthma, hypertension, memory disorders, depression.
XX
PS   Claim 3; Fig 5A; 89pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC   and beta3d subunits. These can be used to identify inhibitors and
CC   activators of the channels, which can be used in the treatment of
CC   conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC   Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC   incontinence, migraine and irritable bowel syndrome. The coding sequences
CC   are found at human chromosome 3q23-ter. The present sequence is the
CC   beta3d subunit coding sequence
XX
SQ   Sequence 1296 BP; 386 A; 274 C; 294 G; 342 T; 0 U; 0 Other;

  Query Match             19.0%;  Score 134.4;  DB 4;  Length 1296;
  Best Local Similarity   54.6%;  Pred. No. 3.7e-31;
  Matches  311;  Conservative    2;  Mismatches  248;  Indels    9;  Gaps    2;

Qy        125 CAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGT 184
              | |||||||||||||||  |  | |||||  | || |||||||  | |||  || | ||||
Db        614 CTGGAGAGGACCGAGCCGTGATGCTGGGGTTTGCCATGATGGGCTTCTCAGTCCTAATGT 673

Qy        185 ATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGT 244
                ||  |||| ||||  ||  | ||     | |  ||||  |||  |   ||  ||||| |
Db        674 TCTTCTTGCTCGGAACAACCATTCTAAAGCCTTTTATGCTCAGCATTCAGAGAGAAGAAT 733

Qy        245 CTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACAT---TTAAYTGCTCCTTCAGCT 301
              |    ||||      |  |  |    |||| |||    |   |  |:||  |||||| ||
Db        734 CGACCTGCACTGCCATCCACACAGATATCATGGACGACTGGCTGGACTGTGCCTTCACCT 793

Qy        302 GTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGA 361
              |||||    |||||      |     |||||| || || |||||||  ||  ||||| |
Db        794 GTGGTGTGCACTGCCACGGTCAGGGGAAGTACCCGTGTCTTCAGGTGTTTGTGAACCTCA 853

Qy        362 CTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGA 421
              | | ||  | ||     |||||  |  | |  ||||||  |  |  | || ||||  |
Db        854 GCCATCCAGGTCAGAAAGCTCTCCTACATTATAATGAAGAGGCTGTCCAGATAAATCCCA 913

Qy        422 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 481
              ||||||  || | ||||||  ||      || ||    | ||  |   |  |    |
Db        914 AGTGCTTTTACACACCTAAGTGCCACCAAGATAGAAATGATTTGCTCAACAGTGCTCTGG 973

Qy        482 TTGTCATGGAAAACTT------CAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAG 535
              | |  |||  |||      ||  ||       | ||| || ||||  |     ||||
Db        974 ACATAAAAGAATTCTTCGATCACAAAAATGGAACCCCCTTTTCATGCTTCTACAGTCCAG 1033

Qy        536 AAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATT 595
              |  |     |  ||| || || | :|||  ||      |  |  | |||||
Db       1034 CCAGCCAATCTGAAGATGTCATTCTTATAAAAAAGTATGACCAAATGGCTATCTTCCACT 1093

Qy        596 CACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAAC 655
              | || |||||  |    |  ||  || ||||     ||||||| ||||||| |
Db       1094 GTTTATTTTGGCCTTCACTGACTCTGCTAGGTGGTGCCCTGATTGTTGGCATGGTGAGAT 1153

Qy        656 TTACACAGTACCTCTCCCTACTATGTGAGA 685
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Db       1154 TAACACAACACCTGTCCTTACTGTGTGAAA 1183


Search completed: November  6, 2004, 23:41:06
Job time : 431 secs
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GenCore version 5.1.6

OM nucleic - nucleic search, using sw model

Run on: November 6, 2004, 23:32:22 ; Search time 2961 Seconds
(without alignments)
8700.740 Million cell updates/sec

Title: US-09-914-053A-6
Perfect score: 707
Sequence: 1 atgtcgatatggaccagtgg.....atccacggatcaatagataa 707

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : EST:*
1: gb_est1:*
2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	692	97.9	801	4	BG188850	BG188850 RST7884 A
	2	649.6	91.9	803	4	BG198614	BG198614 RST17879
	3	642.4	90.9	816	4	BG195580	BG195580 RST14773
	4	626.6	88.6	795	4	BG218411	BG218411 RST38279
	5	604.2	85.5	817	4	BG214809	BG214809 RST34463
	6	584.8	82.7	694	7	CK945448	CK945448 4069809 B
	7	567.2	80.2	2356	3	AK012400	AK012400 Mus muscu
	8	563	79.6	949	5	BQ942589	BQ942589 AGENCOURT
	9	556.8	78.8	1597	3	AK014106	AK014106 Mus muscu
	10	427.4	60.5	855	5	BU216989	BU216989 603107309
c	11	382	54.0	598	7	CK903430	CK903430 ie57a02.x
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	13	349.4	49.4	778	4	BG502844	BG502844 602550401
	14	343.2	48.5	939	5	BU222329	BU222329 603105389
c	15	338.6	47.9	562	2	BF433029	BF433029 7n23h12.x
	16	327.2	46.3	709	7	CK476300	CK476300 AGENCOURT
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	19	300.4	42.5	598	6	CB297668	CB297668 12B22017
	20	298.8	42.3	835	7	CK601161	CK601161 AGENCOURT
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	23	281	39.7	558	1	AA904191	AA904191 oe72h09.s
	24	280	39.6	769	7	CN064012	CN064012 Ag2_p46_A
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	27	233.4	33.0	294	6	CA780337	CA780337 MPL384_6_
c	28	226.6	32.1	446	1	AI299145	AI299145 qm96f01.x
	29	222.4	31.5	992	6	BY713099	BY713099 BY713099
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	37	141.4	20.0	884	7	CF548250	CF548250 AGENCOURT
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	39	134	19.0	885	6	CD516242	CD516242 AGENCOURT
	40	132.8	18.8	847	7	CN232966	CN232966 WLB054C10
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	42	132.4	18.7	784	5	BU483866	BU483866 603847676
	43	131	18.5	666	2	BB632101	BB632101 BB632101
	44	131	18.5	1552	3	AK038987	AK038987 Mus muscu
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ALIGNMENTS

RESULT 1
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LOCUS BG188850 801 bp mRNA linear EST 21-APR-2001
DEFINITION RST7884 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG188850
VERSION BG188850.1 GI:13710537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 554.
FEATURES Location/Qualifiers
source 1. .801
/organism="Homo sapiens"
/mol_type="mRNA"
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/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."
ORIGIN

Query Match 97.9%; Score 692; DB 4; Length 801;
Best Local Similarity 99.3%; Pred. No. 1e-192;
Matches 703; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

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Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db         72 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 131

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        192 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 251

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Db        252 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 311

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        312 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGC 371

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        372 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 431

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Db        432 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 491

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Db        552 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 611

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Db        732 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 779
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RESULT 2
BG198614

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LOCUS       BG198614                803 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST17879 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG198614
VERSION     BG198614.1  GI:13720301
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 553.
FEATURES             Location/Qualifiers
     source          1. .803
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                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN
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Query Match 91.9%; Score 649.6; DB 4; Length 803;
Best Local Similarity 96.6%; Pred. No. 3.3e-180;
Matches 672; Conservative 2; Mismatches 21; Indels 1; Gaps 1;

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Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        193 AAGGCAGGAGAGGAACGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 252

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        433 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 492

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Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGT-GAAACTTAC 659
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Qy        660 ACAGTACCTCTCCCTACTATGTGAGAGGATCCACGG 695
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Db        733 CCAGTCCTTTTCCCTACTATGTGAGAGGATCCACCG 768
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RESULT 3
BG195580
LOCUS       BG195580                816 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST14773 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG195580
VERSION     BG195580.1  GI:13717267
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 816)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 364.
FEATURES             Location/Qualifiers
     source          1. .816
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match           90.9%;  Score 642.4;  DB 4;  Length 816;
  Best Local Similarity  96.7%;  Pred. No. 4.5e-178;
  Matches  671;  Conservative    2;  Mismatches   19;  Indels    2;  Gaps    2;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  ||||||||||||||| ||||||||||||||||||||||||||||||||||||
Db         72 ATGTTTATATGGACCAGTGGCCAGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 131

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 251

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 311

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||||||||||||||||||||||||||||||||||||||||||||:||||||||||||||
Db        312 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGC 371

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 431

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |||||| ||| ||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ACTTCTTNCGGNGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 491

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              ||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||||
Db        492 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTNCCTGGTGAAT 551

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 611

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAA-CGTGCTGTTCCATTCACT 599
              |||||||||||||||| |||||:|||||||||||||||| |||||   ||||||||||
Db        612 AACCAGAAGAGTGTTATNCTAACAAAACTCTACAGTTCCAACCGTGCNTGTCCATTCACT 671

Qy        600 CTTCTGGCCAACCTGTATGAT-GGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTA 658
              |||||| |||||||||||| ||||||||| ||| ||||||||||||||||||||||||
Db        672 TCTCTGGCAAACCTGTATGATGGGCTGGGGGCGTGCAAATTGTTGCCATGGTGAAACTTA 731

Qy        659 CACAGTACCTCTCCCTACTATGTGAGAGGATCCA 692
              ||||| |||||| |||||||||| ||||||||||
Db        732 CACAGGACCTCTNCCTACTATGGGAGAGGATCCA 765


RESULT 4
BG218411
LOCUS       BG218411                795 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST38279 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG218411
VERSION     BG218411.1  GI:13744560
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

  Query Match           88.6%;  Score 626.6;  DB 4;  Length 795;
  Best Local Similarity  96.8%;  Pred. No. 2.1e-173;
  Matches  669;  Conservative    2;  Mismatches   16;  Indels    4;  Gaps    3;
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Qy          2 TGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAATA 61
              |||  |||||||||||| |||||||||||||||||||||||||||||||||||||||||||
Db         73 TGTTTATATGGACCAGCGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAATA 132

Qy         62 TTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTGA 121
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 TTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTGA 192

Qy        122 AGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGA 181
              ||||||||||||||||||| ||||||||||||||||||||||||||||||||||||||||
Db        193 AGGCAGGAGAGGACCGAGCTTTTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGA 252

Qy        182 TGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAG 241
              |||||||||||||||| |    ||||||||||||||||||||||||||||||||||||
Db        253 TGTATTTTCTGCTGGGATT--TCTTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAG 310

Qy        242 AGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGCT 301
              |||||||||||||||||||||||||||||||||||||||||||||:|||||||||||||
Db        311 AGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCT 370

Qy        302 GTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGA 361
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Db        371 GTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGA 430

Qy        362 CTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGA 421
              |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db        431 CTTCTTCCGGGG-AAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGA 489

Qy        422 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 481
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 AGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATG 549

Qy        482 TTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAA 541
              |||||||||||||||| ||||||||||||||| |||||||||||||||||||||||||||
Db        550 TTGTCATGGAAAACTTCACGAAGTATCAACACTTCTTCTGCTATTCTGACCCAGAAGGAA 609

Qy        542 ACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCT 601
              |||||||||||||||||||||:|||||||||||||||||||||||||||||||||||| |
Db        610 ACCAGAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTTT 669

Qy        602 TCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACAC 661
              |||||||||||| |||||||||| || |||||||||||||||||||| ||||| |||||
Db        670 TCTGGCCAACCTGGATGATGGCTGGCGGGGTGGCAATTGTTGCCATGGGGAAAC-TACAC 728

Qy        662 AGTACCTCTCCCTACTATGTGAGAGGATCCA 692
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Db        729 AGTACCTTTCCCTACTATGTGAGAGGATCCA 759
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RESULT 5
BG214809
LOCUS       BG214809                817 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST34463 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG214809
VERSION     BG214809.1  GI:13740830
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 817)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 364.
FEATURES             Location/Qualifiers
     source          1. .817
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN
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Query Match 85.5%; Score 604.2; DB 4; Length 817;
Best Local Similarity 95.6%; Pred. No. 8.5e-167;
Matches 681; Conservative 2; Mismatches 23; Indels 6; Gaps 6;

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Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db         72 ATGTTTATATGGACCAGTGGCCAGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 131

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        192 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 251

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 311

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        312 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGC 371

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        372 TGTGGTCCAGACTGCTGGAAACTNTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 431

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 491

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGT-CCCTGGTGAA 479
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Db        492 AAGTGCTCCTATATACCTANATGTGGAAAAAATTNTGAAGATTCCATGTCCCCTGGTGAA 551

Qy        480 TGTTGTCA-TGGAAAACTTCAGGAAGTATCAACAC-TTCTCCTGCTATTCTGACCCAGAA 537
              |||||||| |||||||||||||||| |||||||| || ||||| ||||||||||||||||
Db        552 TGTTGTCATTGGAAAACTTCAGGAAGGATCAACACTTTTTCCTGTTATTCTGACCCAGAA 611

Qy        538 GGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCA 597
              |||||||||||||||| |||||||||:|||||||||||||||||||| |||||||||| |
Db        612 GGAAACCAGAAGAGTGGTATCCTAACCAAACTCTACAGTTCCAACG-GCTGTTCCATTTA 670

Qy        598 CTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTG-AAACT 656
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Db        671 CTCTTTTGGCCAACCTGTTTGATGGCTGGGGGGCGTGCAATTGTTGCCCTTGTGAAAACT 730

Qy        657 TACACAGTACCTCTCCCTACTATGTGAGAGGATCCA-CGGATCAATAGATAA 707
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Db        731 AACACAGTACCTTTCCCTACTATGTGAGAGGATCCACCGGATCAATAAATAA 782
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RESULT 6
CK945448
LOCUS       CK945448                694 bp    mRNA    linear   EST 15-MAR-2004
DEFINITION  4069809 BARC 10BOV Bos taurus cDNA clone 10BOV17_N10 5', mRNA
            sequence.
ACCESSION   CK945448
VERSION     CK945448.1  GI:45459828
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 694)
  AUTHORS   Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
  TITLE     Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt " -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 17  row: N  column: 10
            Seq primer: CCCAGTCACGACGTTGTAAAACG
            High quality sequence stop: 694.
FEATURES             Location/Qualifiers
     source          1. .694
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                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="10BOV17_N10"
                     /sex="Male"
                     /tissue_type="Pooled"
                     /dev_stage="Multiple"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="BARC 10BOV"
                     /note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
                     EcoRV; Site_2: NotI; Equimolar amounts of mRNA extracted
                     from proximal jejunums of 18 and 21 wk old steers, and
                     distal ileums of 14 day old calves. proximal jejunum
                     exposed to C. oncophora for 3 and 6 weeks, and distal
                     ileum exposed to C. parvum for 7 days"
ORIGIN

  Query Match           82.7%;  Score 584.8;  DB 7;  Length 694;
  Best Local Similarity  93.6%;  Pred. No. 4.3e-161;
  Matches  629;  Conservative    2;  Mismatches   39;  Indels    2;  Gaps    2;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
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Db         17 ATGTTTATATGGACCAGTGGCCGGACTTCTTCATCTTACAGACATGATGAGAAAAGAAAT 76

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              |||||||| |||||||||||||| |||||||||||||||||||| ||||||||||||
Db         77 ATTTACCAAAAAATCAGGGACCACGACCTCCTGGACAAAAGGAAAACTGTCACAGCACTG 136

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              || |||||||||||||| || |||||||||||||||||| ||||||||||||||||||||
Db        137 AAAGCAGGAGAGGACCGGGCCATTCTCCTGGGACTGGCCATGATGGTGTGCTCCATCATG 196

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Db        197 ATGTACTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGTGTATGGACCGAG 256

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
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Db        257 GAGGCTCAGTGCACCTTGCTGAATGCATCCATCACAGAAACATTTAACTGCTCCTTCAGC 316

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        317 TGTGGTCCGGACTGCTGGAAACTCTCTCAGTATCCCTGCCTACAGGTGTATGTTAACCTG 376

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Db        377 ACTTCTTCCGGTGAAAAGCTCCTTCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 436

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Db        437 AAGTGCTCCTATATACCTAAGTGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 496

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Db        497 GTTGTCATGGAAAACTTCAGGAAGTACCAACACTTCTCCTGCTACTCTGACCCGGAAGGA 556

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
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Db        557 AACCAGAAGAGTGTCATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 616

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
              || |||||||| |||||||||||||| |||||||||| |||||||||| |||| |||
Db        617 TTTGGCCAACATGCATGATGGCTGGGGGCGTGGCAATTG-TGCCATGGTG-AACTCACA 674

Qy        661 CAGTACCTCTCC 672
              ||||| || |||
Db        675 CAGTATCTTTCC 686


RESULT 7
AK012400
LOCUS       AK012400                2356 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 11 days embryo whole body cDNA, RIKEN full-length
            enriched library, clone:2700049B16 product:LARGE CONDUCTANCE
            CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT, full insert sequence.
ACCESSION   AK012400
VERSION     AK012400.1  GI:12849119
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
```

AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2356)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

FEATURES Location/Qualifiers
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/clone="2700049B16"
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polyA_site 2356
/note="putative"

ORIGIN

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Best Local Similarity 88.3%; Pred. No. 1.1e-155;
Matches 625; Conservative 2; Mismatches 80; Indels 1; Gaps 1;

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Db        242 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 301

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
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Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db        902 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGATAA 949
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RESULT 8
BQ942589
LOCUS BQ942589 949 bp mRNA linear EST 21-AUG-2002
DEFINITION AGENCOURT_8888599 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311623 5', mRNA sequence.
ACCESSION BQ942589
VERSION BQ942589.1 GI:22358067
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 949)
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov

```
            Tissue Procurement: Susan L. Sullivan, PhD.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13735  row: n  column: 08
            High quality sequence start: 36
            High quality sequence stop: 564.
FEATURES             Location/Qualifiers
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                     /clone_lib="NIH_MGC_129"
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                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
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                     by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
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ORIGIN

  Query Match             79.6%;  Score 563;  DB 5;  Length 949;
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Qy        365 CTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGT 424
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RESULT 9
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LOCUS       AK014106               1597 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
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            CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT, full insert sequence.
ACCESSION   AK014106
VERSION     AK014106.1  GI:12851769
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
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            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1597)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
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            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
```

RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)

COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
Host: SOLR.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6J"
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/db_xref="taxon:10090"
/clone="3110031N04"
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/dev_stage="13 days embryo"
misc_feature 488. .1194
/note="LARGE CONDUCTANCE CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT (SPTR|AAL38982, evidence: FASTY, 100%ID, 100%length, match=705)
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ORIGIN

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Best Local Similarity 88.3%; Pred. No. 1.1e-152;
Matches 625; Conservative 2; Mismatches 79; Indels 2; Gaps 2;

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Db        488 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 547

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
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Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
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Db        728 GAG-CCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 786

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
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Db        787 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 846

Qy        361 ACTTCTTCCGGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
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Db        847 ACATCTTCCGGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 906

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
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Db        907 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 966

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
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Db       1027 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 1086

Qy        601 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 660
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Db       1087 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 1146

Qy        661 CAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
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Db       1147 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGATAA 1194
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RESULT 10
BU216989
LOCUS BU216989 855 bp mRNA linear EST 25-NOV-2002
DEFINITION 603107309F1 CSEQCHN04 Gallus gallus cDNA clone ChEST48b4 5', mRNA sequence.
ACCESSION BU216989
VERSION BU216989.1 GI:25398033
KEYWORDS EST.
SOURCE Gallus gallus (chicken)
ORGANISM Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae; Gallus.
REFERENCE 1 (bases 1 to 855)
AUTHORS Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E., Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
TITLE A Comprehensive Collection of Chicken cDNAs
JOURNAL Curr. Biol. 12 (22), 1965-1969 (2002)
MEDLINE 22335534
PUBMED 12445392
COMMENT Contact: Simon Hubbard
Department of Biomolecular Sciences
University of Manchester Institute of Science and Technology (UMIST)
PO Box 88, Manchester, M60 1QD, UK
Tel: 01612008930
Fax: 01612360409
Email: Simon.Hubbard@umist.ac.uk.

FEATURES Location/Qualifiers
source 1. .855
/organism="Gallus gallus"
/mol_type="mRNA"
/strain="White Leghorn, Hisex"
/db_xref="taxon:9031"
/clone="ChEST48b4"
/tissue_type="whole embryo"
/dev_stage="20-21"
/lab_host="DH10B"
/clone_lib="CSEQCHN04"
/note="Organ: whole embryo; Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: Not1; This normalized library was constructed from 1 million independent clones. cDNA synthesis was initiated using an oligo(dT) primer, using methylated C in the first strand synthesis reaction. Following this first strand reaction, double-stranded cDNA was blunted, ligated to NotI adapters, digested with EcoRI, size-selected, and cloned into the NotI and EcoRI compatible sites of a custom modified MCS of the pBluescript (KS+) vector. The library was normalized in 2 rounds using conditions adapted from Soares et al., PNAS (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6 (1996): 791, except that a significantly longer reannealing hybridization was used."

ORIGIN

Query Match 60.5%; Score 427.4; DB 5; Length 855;
Best Local Similarity 78.4%; Pred. No. 1.4e-114;

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  Matches  556;  Conservative    2;  Mismatches  128;  Indels   23;  Gaps    3;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  ||  ||||||||||||||||| |||| ||||||| ||||| ||||| |||
Db        152 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 205

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
                         ||||| || || || ||||||||||||||||||||||| ||
Db        206 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 250

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              || || ||||| ||||| || || ||||| || ||||| |||||||||||||| ||||||
Db        251 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 310

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||| ||||| |||||||||| || ||||| || |||||||||||||| ||||| |||
Db        311 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 370

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||| |||| ||| |  |  || || |||||||| ||||| || ||:||||| || |||
Db        371 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 430

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              || || ||||||||||||||| | |||||||||||||||| |||||||||||| || ||
Db        431 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 490

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 420
              |||||||| ||  | ||||| || |||||||||| ||||| ||||| |||| |||
Db        491 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 550

Qy        421 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 480
              |||| || || ||||| || ||||| || |||| || |||||||||| |||||||
Db        551 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 610

Qy        481 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 540
              ||||| |||||||||||| | |||||||||| |||||||||| | ||| || || ||
Db        611 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 670

Qy        541 AACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 600
              |  |||||||  || ||  | ||:||||| ||||| |||||||||||||||| || |||
Db        671 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 730

Qy        601 TTCTGGCCAACCTGTATGATG-GCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTAC 659
              |||||||| || || ||||||  | | ||  || || |||||||| |||| || || ||
Db        731 TTCTGGCCCACGTGCATGATGATCGGCGGCCGTTGCCATTGTTGCGATGGTAAAGCTGAC 790

Qy        660 ACAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
                || ||||| || || || || ||||| |||| | ||||||| ||||||
Db        791 TCAATACCTTTCTCTCCTCTGGGAGAGAATCCAAAGGATCAACAGATAA 839


RESULT 11
CK903430/c
LOCUS       CK903430                598 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  ie57a02.x5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            cDNA clone IMAGE:5670818 3' similar to TR:Q9Y691 Q9Y691 MAXIK
            CHANNEL BETA 2 SUBUNIT. ;, mRNA sequence.
ACCESSION   CK903430
VERSION     CK903430.1  GI:45364961
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ie57a02.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 3' RESEQUENCE of a previously sequenced pancreas
            clone
            This resequenced clone has not previously been sequenced on this
            end, resequencing from this end represents new data
            Seq primer: -40UP from Gibco
            High quality sequence stop: 584.
FEATURES             Location/Qualifiers
     source          1. .598
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5670818"
                     /sex="Both"
                     /tissue_type="Islets of Langerhans"
                     /dev_stage="Adult"
                     /lab_host="DH10B"
                     /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                     /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
                     Site_2: Sal 1; Starting library constructed using
                     SuperScript Plasmid Library kit (Life Technologies). cDNA
                     made by oligo-dT priming. Size-selected by column
                     fractionation; average insert size 1.08 kb. Library was
                     amplified once on solid support and plasmid DNA from
                     library was prepared. The library DNA was normalized by
                     method #4 from Bonaldo, Lennon, and Soares 1996 Genome
                     Research 6:791-806; 0.5 microgram single-stranded library
                     plasmid DNA was mixed with 5 micrograms PCR product
                     representing library inserts and hybridized to an Ecot of
                     20. Single-stranded (unhybridized) plasmids were isolated
                     by hydroxyapatite chromatography and used to make this
                     library."
ORIGIN

  Query Match             54.0%;  Score 382;  DB 7;  Length 598;
  Best Local Similarity   99.2%;  Pred. No. 3.2e-101;
  Matches  393;  Conservative    1;  Mismatches    1;  Indels    1;  Gaps    1;

Qy        313 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 372
              |||||||| ||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 TGCTGGAAATTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 539

Qy        373 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 432
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 479

Qy        433 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 492
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 419

Qy        493 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 552
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 359

Qy        553 GTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 612
              ||||||||||:||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 299

Qy        613 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 672
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 239

Qy        673 CTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||| ||||||||||||||||
Db        238 CTACTATGTGAGAGGATCCAACGGATCAATAGATAA 203
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RESULT 12
BU950136/c
LOCUS       BU950136                622 bp    mRNA    linear   EST 21-OCT-2002
DEFINITION  io77a08.x1 HR85 islet Homo sapiens cDNA clone IMAGE:6132374 3'
            similar to TR:Q9Y691 Q9Y691 MAXIK CHANNEL BETA 2 SUBUNIT. ;, mRNA
            sequence.
ACCESSION   BU950136
VERSION     BU950136.1  GI:24201487
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 622)
  AUTHORS   Melton,D., Brown,J., Kenty,G., Permutt,A., Lee,C., Kaestner,K.,
            Lemishka,I., Sceare,M., Brestelli,J., Gradwohl,G., Clifton,S.,
            Hillier,L., Marra,M., Pape,D., Wylie,T., Martin,J., Blistain,A.,
            Schmitt,A., Theising,B., Ritter,E., Ronko,I., Bennett,J.,
            Cardenas,M., Gibbons,M., McCann,R., Cole,R., Tsagareishvili,R.,
            Williams,T., Jackson,Y. and Bowers,Y.
  TITLE     Endocrine Pancreas Consortium
  JOURNAL   Unpublished (2000)
COMMENT     Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            Library was constructed by Dr. Hiroshi Inoue DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: Dr. Hiroshi Inoue
            (hinoue@im.wustl.edu)
            Seq primer: -40UP from Gibco
            High quality sequence stop: 293.
FEATURES             Location/Qualifiers
     source          1. .622
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:6132374"
                     /tissue_type="Purified pancreatic islet"
                     /lab_host="DH10B"
                     /clone_lib="HR85 islet"
                     /note="Organ: Pancreas; Vector: pBluescript SK(-); Site_1:
                     NotI; Site_2: XhoI; cDNA made by oligo-dT priming.
                     Size-selected on agarose gel. Average insert size ~1kb. 5'
                     XhoI site was destroyed after directional cloning.
                     Amplified once. Contact information: Hiroshi Inoue, MD,
                     Metabolism Div. (Alan Permutt Lab), Washington University
                     School of Medicine, Box 8127, 660 South Euclid Ave., St.
                     Louis, MO 63110, E-mail: hinoue@imgate.wustl.edu, Tel:
                     314-362-1916, Fax: 314-747-2692."
ORIGIN

  Query Match           51.3%;  Score 362.8;  DB 5;  Length 622;
  Best Local Similarity   92.9%;  Pred. No. 1.5e-95;
  Matches  390;  Conservative    1;  Mismatches   28;  Indels    1;  Gaps    1;

Qy        289 TGCTCCTTCAGCTGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTG 348
              ||||||||    |||||||||||||| |||||||||| |||| ||||||||  |  ||||
Db        622 TGCTCCTTGCAGTGTGGTCCAGACTCCTGGAAACTTTGTCAGGACCCCTGCTCCAGGGTG 563

Qy        349 TACGTTAACCTGACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATA 408
              | |||||||||| ||| ||| || |||||| ||||||| |||||| ||||||||||||||
Db        562 TGCGTTAACCTGTCTTTTTCGGGCGAAAAGGTCCTCCTTTACCACCCAGAAGAGACAATA 503

Qy        409 AAAATCAATCAGAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATG 468
              |||||||||||| |||||||||||||||||||||||||||||||||||||||||||||||
Db        502 TAAATCAATCAGAGGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATG 443

Qy        469 TCCCTGGTGAATGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCT 528
              ||||||||||||||||||||||||||||||||||||||||||||| ||||||||||||||
Db        442 TCCCTGGTGAATGTTGTCATGGAAAACTTCAGGAAGTATCACCACTTCTCCTGCTATTCT 383

Qy        529 GACCCAGAAGGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTG 588
              ||||||||||||||||||||||||||||||||||:|||||||||||||||||||||||||
Db        382 GACCCAGAAGGAAACCAGAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTG 323

Qy        589 TTCCATTCACTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATG 648
              |||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 TTCCATTCACTGTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATG 263

Qy        649 GTGAAACTTACACAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||| |||| ||||||||| |||||||||  |||| ||||||||||||||||
Db        262 GTGAAACTTACGCAGTGCCTCTCCCTGCTATGTGAGAAAATCCAACGGATCAATAGATAA 203


RESULT 13
BG502844
LOCUS       BG502844                778 bp    mRNA    linear   EST 27-MAR-2001
DEFINITION  602550401F1 NIH_MGC_61 Homo sapiens cDNA clone IMAGE:4657825 5',
            mRNA sequence.
ACCESSION   BG502844
VERSION     BG502844.1  GI:13464361
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 778)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
             cDNA Library Preparation: CLONETECH Laboratories, Inc.
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Incyte Genomics, Inc.
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLCM1451  row: b  column: 02
            High quality sequence stop: 759.
FEATURES             Location/Qualifiers
     source          1. .778
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:4657825"
                     /tissue_type="embryonal carcinoma"
                     /lab_host="DH10B (T1 phage-resistant)"
                     /clone_lib="NIH_MGC_61"
                     /note="Organ: testis; Vector: pDNR-LIB (Clontech); Site_1:
                     SfiI (ggccgcctcggcc); Site_2: SfiI (ggccattatggcc);
                     Double-stranded cDNA was prepared from cell line RNA.  5'
                     and 3' adaptors were used in cloning as follows: 5'
                     adaptor sequence:  5'-CACGGCCATTATGGCC-3' and 3' adaptor
                     sequence:  5'-ATTCTAGAGGCCGAGGCGGCCGACATG-dT(30)BN-3'
                     (where B = A, C, or G and N = A, C,  G, or T).  Average
                     insert size 1.75 kb (range 0.9-4.0 kb). 15/15 colonies
                     contained  inserts by PCR. This library was enriched for
                     full-length clones and was constructed by Clontech
                     Laboratories (Palo Alto, CA). Note: this is a NIH_MGC
                     Library."
ORIGIN

  Query Match           49.4%;  Score 349.4;  DB 4;  Length 778;
  Best Local Similarity   94.9%;  Pred. No. 1.5e-91;
  Matches  392;  Conservative    1;  Mismatches   17;  Indels    3;  Gaps    3;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
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Db        344 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 403

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        404 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 463

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        464 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 523

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGT-GTGGACCGA 239
              ||||||||||||||||||||||||||||||||||||||||||||||||| |||||||||
Db        524 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGGTGGACCGA 583

Qy        240 AGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAG 299
              ||||||||||||||||||||||||||||||||||||||||||||||:||||||||||||
Db        584 AGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAG 643

Qy        300 CTGTGGTCCAGACTGCTGGAAAC-TTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACC 358
              ||||||||||||||||||||||| |||||||||||||||||  |  |      |||||||
Db        644 CTGTGGTCCAGACTGCTGGAAACTTTTCTCAGTACCCCTGCTCCAGGTGTACCGTTAACC 703

Qy        359 TGACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAA 411
              |||||||||||||||||||  ||  | |||||||  |||||||| ||| |||||
Db        704 TGACTTCTTCCGGGGAAAAGTTCTCCTTCTACCA-ACAGAAGAAACATTAAAA 755
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RESULT 14
BU222329

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LOCUS       BU222329                939 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  603105389F1 CSEQCHN04 Gallus gallus cDNA clone ChEST43b24 5', mRNA
            sequence.
ACCESSION   BU222329
VERSION     BU222329.1  GI:25411618
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="ChEST43b24"
                     /tissue_type="whole embryo"
                     /dev_stage="20-21"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN04"
                     /note="Organ: whole embryo; Vector: pBluescript II KS(+);
                     Site_1: EcoRI; Site_2: Not1; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN
```

```
  Query Match             48.5%;  Score 343.2;  DB 5;  Length 939;
  Best Local Similarity   78.2%;  Pred. No. 1.1e-89;
  Matches  444;  Conservative    2;  Mismatches  100;  Indels   22;  Gaps    2;

Qy          1 ATGTCGATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 60
              ||||  || |||||||||||||||| |||| ||||||| ||||| ||||| |||
Db        152 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 205

Qy         61 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 120
                         ||||| || || || |||||||||||||||||||||||||| ||
Db        206 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 250

Qy        121 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 180
              || || ||||| ||||| || || ||||| || ||||| |||||||||||||| ||||||
Db        251 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 310

Qy        181 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 240
              ||||| ||||| |||||||||| || ||||| || |||||||||||||| ||||| |||
Db        311 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 370

Qy        241 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAAYTGCTCCTTCAGC 300
              ||| |||| ||| |  | || || || |||||||| ||||| || ||:||||| || |||
Db        371 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 430

Qy        301 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 360
              || || |||||||||||||||| | |||||||||||||||| |||||||||||  || ||
Db        431 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 490

Qy        361 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAAT-AAAAATCAATCA 419
              |||||||| ||  | ||||| || |||||||||| ||||| ||||| ||| || |||
Db        491 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAACATTAATTC 550

Qy        420 GAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAA 479
              |||| || || ||||| || ||||| || ||||  || |||||||||||  |||||||
Db        551 TGAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAA 610

Qy        480 TGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGG 539
              ||||| |||||||||||| | |||||||||| ||||||||||  | ||| || || ||
Db        611 CGTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGG 670

Qy        540 AAACCAGAAGAGTGTTATCCTAACMAAA 567
              |  |||||||  || ||  | ||:|||
Db        671 CACTCAGAAGAACGTGATATTGACCAAA 698
```

RESULT 15
BF433029/c

```
LOCUS       BF433029                562 bp    mRNA    linear   EST 29-NOV-2000
DEFINITION  7n23h12.x1 NCI_CGAP_Lu24 Homo sapiens cDNA clone IMAGE:3565679 3'
            similar to TR:Q9Y691 Q9Y691 MAXIK CHANNEL BETA 2 SUBUNIT. ;, mRNA
            sequence.
ACCESSION   BF433029
VERSION     BF433029.1  GI:11445192
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 562)
  AUTHORS   NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
  TITLE     National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
            Tumor Gene Index
  JOURNAL   Unpublished (1997)
COMMENT     Contact: Robert Strausberg, Ph.D.
```

Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher Moskaluk, M.D., Ph.D., Michael R. Emmert-Buck, M.D., Ph.D.
cDNA Library Preparation: M. Bento Soares, Ph.D.
cDNA Library Arrayed by: Greg Lennon, Ph.D.
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL, send email to: info@image.llnl.gov
Seq primer: -40UP from Gibco
High quality sequence stop: 498.

FEATURES Location/Qualifiers
source 1. .562
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:3565679"
/tissue_type="carcinoid"
/lab_host="DH10B"
/clone_lib="NCI_CGAP_Lu24"
/note="Organ: lung; Vector: pT7T3D-Pac (Pharmacia) with a modified polylinker; Plasmid DNA from the normalized library NCI_CGAP_Lu5 was prepared, and ss circles were made in vitro. Following HAP purification, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNAs from a pool of 5,000 clones made from the same library (cloneIDs 1414920-1417991 and 1520904-1522439). Subtraction by Bento Soares and M. Fatima Bonaldo. "

ORIGIN

Query Match 47.9%; Score 338.6; DB 2; Length 562;
Best Local Similarity 99.4%; Pred. No. 2e-88;
Matches 349; Conservative 1; Mismatches 0; Indels 1; Gaps 1;

```
Qy        358 CTGACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAAT 417
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        562 CTGACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAAT 503

Qy        418 CAGAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTG 477
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        502 CAGAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTG 443

Qy        478 AATGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAA 537
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        442 AATGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAA 383

Qy        538 GGAAACCAGAAGAGTGTTATCCTAACMAAACTCTACAGTTCCAACGTGCTGTTCCATTCA 597
              |||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||
Db        382 GGAAACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCA 323

Qy        598 CTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTT 657
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        322 CTCTTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTT 263

Qy        658 ACACAGTACCTCTCCCTACTATGTGAGAGGATCC-ACGGATCAATAGATAA 707
              |||||||||||||||||||||||||||||||| ||||||||||||||||
Db        262 ACACAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGATAA 212
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Search completed: November 7, 2004, 01:24:17
Job time : 2971 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 6, 2004, 23:27:01 ; Search time 16 Seconds
(without alignments)
1413.184 Million cell updates/sec

Title: US-09-914-053A-5
Perfect score: 1241
Sequence: 1 MSIWTSGRTSSSYRHDEKRN.....MVKLTQYLSLLCERIQRINR 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR_79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	421	33.9	191	2	S68842	calcium-regulated
2	382	30.8	191	2	A54165	charybdotoxin rece
3	93.5	7.5	255	2	T25853	hypothetical prote
4	89	7.2	286	1	C42053	gap junction prote
5	89	7.2	359	1	HLHUB4	MHC class I histoc
6	89	7.2	362	2	I37519	MHC class I histoc
7	88	7.1	362	2	I61861	MHC HLA-B44.2 chai
8	87.5	7.1	1880	2	T18531	tractin - medicina
9	87	7.0	398	2	F90206	histidinol dehydro
10	87	7.0	497	2	G87793	protein C27A12.7 [
11	86	6.9	238	2	B36284	prolactin-like pro
12	85.5	6.9	491	2	F87793	protein C27A12.6 [
13	84.5	6.8	422	2	S24451	hypothetical prote
14	84	6.8	362	2	C35997	MHC class I histoc
15	83	6.7	362	2	I38421	gene HLA B-1519 pr
16	83	6.7	1562	2	T07323	DNA-directed RNA p
17	83	6.7	1589	1	RGBYC5	cell division cont
18	82.5	6.6	247	2	A86809	hypothetical prote
19	82	6.6	336	2	T21531	hypothetical prote
20	82	6.6	350	2	I54308	MHC HLA B71 - huma
21	82	6.6	354	2	S24433	class I histocompa
22	82	6.6	362	2	I84486	transmembrane glyc
23	82	6.6	362	2	I62042	MHC HLA-B cell sur
24	82	6.6	362	2	G01230	MHC class I histoc
25	82	6.6	362	2	I59654	major histocompati
26	82	6.6	362	2	I62045	gene HLA B-1517 pr
27	82	6.6	362	2	I61863	MHC HLA-Bw46 - hum
28	82	6.6	362	2	S77966	MHC class I histoc
29	82	6.6	362	2	I37520	MHC class I histoc
30	82	6.6	362	2	I62041	MHC HLA-B cell sur
31	82	6.6	362	2	I62044	MHC class I histoc
32	82	6.6	362	2	S16789	class I histocompa
33	81.5	6.6	668	2	T08725	probable finger pr
34	81.5	6.6	1091	2	T30256	calcium channel al
35	81.5	6.6	1314	2	T30300	dynein heavy chain
36	81	6.5	710	2	T25734	hypothetical prote
37	80.5	6.5	366	2	I37078	HLA-C alpha chain
38	80	6.4	358	2	S75232	hypothetical prote
39	80	6.4	362	2	I62043	MHC HLA-B cell sur
40	80	6.4	436	2	H87793	protein C27A12.8 [
41	80	6.4	3744	2	S46715	hypothetical prote
42	79.5	6.4	345	2	T16074	hypothetical prote
43	79.5	6.4	368	2	C90558	lipoprotein [impor
44	79.5	6.4	849	2	T22306	hypothetical prote
45	79.5	6.4	969	2	T38478	RhoGAP/LIM domain

ALIGNMENTS

RESULT 1
S68842
calcium-regulated potassium channel beta chain - human
C;Species: Homo sapiens (man)
C;Date: 04-Dec-1997 #sequence_revision 12-Dec-1997 #text_change 09-Jul-2004
C;Accession: S68842; S62905
R;Meera, P.; Wallner, M.; Jiang, Z.; Toro, L.
FEBS Lett. 385, 124-131, 1996
A;Title: Corrigendum to: a calcium switch for the functional coupling between alpha (hslo
A;Reference number: S68842
A;Accession: S68842
A;Molecule type: mRNA
A;Residues: 1-191 <MEE>
A;Cross-references: UNIPROT:Q16558
R;Meera, P.; Wallner, M.; Jiang, Z.; Toro, L.
FEBS Lett. 382, 84-88, 1996
A;Title: A calcium switch for the functional coupling between alpha (hslo) and beta subur
A;Reference number: S62904; MUID:96196569; PMID:8612769
A;Accession: S62905
A;Status: nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-165,'L',167-191 <MEW>
A;Cross-references: EMBL:U25138

Query Match 33.9%; Score 421; DB 2; Length 191;
Best Local Similarity 43.0%; Pred. No. 8.5e-31;
Matches 83; Conservative 40; Mismatches 62; Indels 8; Gaps 2;

```
Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | | || ||: ||: |:||::: |::|  |:|  | :||||:||:| |:  :| :
Db          3 KKLVMAQKRGETRALCLGVTMVVCAVITYYILVTTVLPLYQKSVWTQESKCHLIETNIRD 62

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                        |: ||||| :||:::: |  :|||||:|   ||:|||||    |::
Db         63 QEELKGK------KVPQYPCL--WVNVSAAGRWAVLYHTEDTRDQNQQCSYIPGSVDNYQ 114

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               : : |  |  |:: | | |:| | ||: ||:  :||    |  ||||| :: ||: |
Db        115 TARADVEKVRAKFQEQQVFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPTFLLTGGLLI 174

Qy        214 VAMVKLTQYLSLL 226
              :|||| ||||:|
Db        175 IAMVKSNQYLSIL 187
```

RESULT 2
A54165
charybdotoxin receptor beta chain - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 02-Aug-1994 #sequence_revision 02-Aug-1994 #text_change 09-Jul-2004
C;Accession: A54165
R;Knaus, H.G.; Folander, K.; Garcia-Calvo, M.; Garcia, M.L.; Kaczorowski, G.J.; Smith, M

J. Biol. Chem. 269, 17274-17278, 1994
A;Title: Primary sequence and immunological characterization of beta-subunit of high con
A;Reference number: A54165; MUID:94274724; PMID:8006036
A;Accession: A54165
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-191 <KNA>
A;Cross-references: UNIPROT:Q28067; GB:L26101; NID:g508845; PIDN:AAA21741.1; PID:g508846

Query Match 30.8%; Score 382; DB 2; Length 191;
Best Local Similarity 40.4%; Pred. No. 2.9e-27;
Matches 78; Conservative 39; Mismatches 68; Indels 8; Gaps 2;

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Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
Db          3 KKLVMAQRRGETRALCLGVAMVVGAVITYYILGTTVLPLYQKSVWTQESTCHLIETNIRD 62

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
Db         63 QEELEGK------RVPQYPCL--WVNVSSVGRWAVLYHTEDTRDQNHQCSYIPSSLDNYQ 114

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
Db        115 VARADVEKVRARFHENQDFFCFSTTRENETSVLYRRLYGPQSLLFSLFWPTFLLTGGLLI 174

Qy        214 VAMVKLTQYLSLL 226
Db        175 IVMVKINQSLSIL 187
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RESULT 3
T25853
hypothetical protein T01B11.7 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T25853
R;Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996
A;Description: The sequence of C. elegans cosmid T01B11.
A;Reference number: Z20099
A;Accession: T25853
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-255 <GEI>
A;Cross-references: UNIPROT:Q9NJF1; EMBL:U80931; PIDN:AAB38004.1; GSPDB:GN00022; CESP:T0
A;Experimental source: strain Bristol N2; clone T01B11
C;Genetics:
A;Gene: CESP:T01B11.7
A;Map position: 4
A;Introns: 72/1; 114/3; 154/3; 195/2; 214/3

Query Match 7.5%; Score 93.5; DB 2; Length 255;
Best Local Similarity 20.2%; Pred. No. 0.57;
Matches 52; Conservative 42; Mismatches 88; Indels 75; Gaps 10;

```
Qy          6 SGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLL 65
Db          2 SSKSSTSSEEDE--NFIKDVEDQKVLEVLTSHSKFKSLDDLVELRWYCMLV--LIMAEIT 57

Qy         66 GITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGE 125
Db         58 AFTALASVMVMVFAGANP-TVVGCDNTVVNGC---------------------------- 88

Qy        126 KLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQH-------------- 171
Db         89 -----HEYYSLKNRSGCT--PVLEYQFESVQVEFNYICDDAKKVKNTITIQTFGVLVGAA 141

Qy        172 -FSCYSDPEGNQKSVILTKL----------YSSNVLFHSLFWPTC--MMAGGVAIVAMVK 218
Db        142 IFGQVSDNFGRRKALIISCIGNAIFNLISSYSPS-LFYFMLWRTVSGIFAGGLTVVQMV- 199

Qy        219 LTQYLSLLCERIQRINR 235
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Db 200 ------YMVENIPRHHR 210

RESULT 4
C42053
gap junction protein Cx33 - rat
N;Alternate names: connexin 33
C;Species: Rattus norvegicus (Norway rat)
C;Date: 04-Mar-1993 #sequence_revision 02-Jun-1994 #text_change 09-Jul-2004
C;Accession: C42053
R;Haefliger, J.A.; Bruzzone, R.; Jenkins, N.A.; Gilbert, D.J.; Copeland, N.G.; Paul, D.L.
J. Biol. Chem. 267, 2057-2064, 1992
A;Title: Four novel members of the connexin family of gap junction proteins. Molecular cl
A;Reference number: A42053; MUID:92112940; PMID:1370487
A;Accession: C42053
A;Molecule type: DNA
A;Residues: 1-286 <HAE>
A;Cross-references: UNIPROT:P28233; GB:M76534; NID:g203663; PIDN:AAA40998.1; PID:g203664
A;Note: sequence extracted from NCBI backbone (NCBIP:76095)
C;Superfamily: gap junction protein
C;Keywords: gap junction; phosphoprotein; transmembrane protein
F;1-23/Domain: intracellular #status predicted <INT1>
F;24-41/Domain: transmembrane #status predicted <TM1>
F;42-77/Domain: extracellular #status predicted <EE1>
F;78-97/Domain: transmembrane #status predicted <TM2>
F;98-150/Domain: intracellular #status predicted <INT2>
F;151-187/Domain: transmembrane #status predicted <TM3>
F;188-207/Domain: extracellular #status predicted <EE2>
F;208-234/Domain: transmembrane #status predicted <TM4>
F;235-286/Domain: intracellular #status predicted <INT3>

Query Match 7.2%; Score 89; DB 1; Length 286;
Best Local Similarity 23.9%; Pred. No. 1.7;
Matches 37; Conservative 26; Mismatches 66; Indels 26; Gaps 7;

```
Qy         59 IMMYFLLGITLLRSYMQSVWTEES---QCTLLNASITETFNCSFSCGPDCWKLSQYPCLQ 115
Db         26 IKVLFIFRILLLGTAIESAWSDEQFEFHCN------TQQPGCENVCYDQAFPISHVRLWV 79

Qy        116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNV----VMENFRKY-- 169
Db         80 LQVIFVSVPTLLHLAHVYYVIRQNEKLK------KQEEEELKVAHFNGASGERRLQKHTG 133

Qy        170 QHFSCYSDPEGNQK---SVILTKLYSSNVLFHSLF 201
Db        134 KHIKCGSKEHGNRKMRGRLLLT--YMASIFFKSVF 166
```

RESULT 5
HLHUB4
MHC class I histocompatibility antigen HLA-B44 alpha chain precursor - human (fragment)
C;Species: Homo sapiens (man)
C;Date: 31-Dec-1988 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004
C;Accession: A25295
R;Kottmann, A.H.; Seemann, G.H.A.; Guessow, H.D.; Roos, M.H.
Immunogenetics 23, 396-400, 1986
A;Title: DNA sequence of the coding region of the HLA-B44 gene.
A;Reference number: A25295; MUID:86249389; PMID:3459708
A;Accession: A25295
A;Molecule type: mRNA
A;Residues: 1-359 <KOT>
A;Cross-references: UNIPROT:P30481; GB:M15470; NID:g187680; PIDN:AAA59619.1; PID:g386883
C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: duplication; glycoprotein; heterodimer; transmembrane protein; transplantatic
F;1-21/Domain: signal sequence (fragment) #status predicted <SIG>
F;22-359/Product: class I histocompatibility antigen HLA-B44 alpha chain #status predicte
F;22-304/Domain: extracellular #status predicted <EXT>
F;22-111/Domain: alpha-1 <EX1>
F;112-203/Domain: alpha-2 <EX2>

```
F;217-282/Domain: immunoglobulin homology <IMM>
F;305-328/Domain: transmembrane #status predicted <TMM>
F;329-359/Domain: intracellular #status predicted <INT>
F;107/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.2%;  Score 89;  DB 1;  Length 359;
  Best Local Similarity   21.3%;  Pred. No. 2.2;
  Matches   50;  Conservative   37;  Mismatches   88;  Indels   60;  Gaps   10;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              :| ||:  |::                  : :||   |  | :||| | ||
Db        151 LSSWTAADTAAQ-----------------ITQRKWEAARVAEQDRAYLEGLC------- 185

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPD-----CWKLSQYPCLQ 115
                    :  || |:     |  : ||  |   :|                || |  ||  :
Db        186 ------VESLRRYL-----ENGKETLQRADPPKTHVTHHPISDHEATLRCWSLGFYPA-E 233

Qy        116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCY 175
              : :      ||      |::|  :  :    |   : |::  ::|     |      | ::|:
Db        234 ITLTWQRDGED----QTQDTELVETR----PAGDRTFQKWAAVVVPSGEE----QRYTCH 281

Qy        176 SDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYL-SLLCER 229
                ||  | : |    ||          |   :  |:|::|:| :   : :::| |
Db        282 VQHEGLPKPLTLRWEPSSQSTV-----PIVGIVAGLAVLAVVVIGAVVAAVMCRR 331


RESULT 6
I37519
MHC class I histocompatibility antigen HLA-B45 alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I37519; S16772
R;Madrigal, J.A.; Belich, M.P.; Hildebrand, W.H.; Benjamin, R.J.; Little, A.M.; Zemmour,
J. Immunol. 149, 3411-3415, 1992
A;Title: Distinctive HLA-A,B antigens of black populations formed by interallelic conver
A;Reference number: I37476; MUID:93056508; PMID:1431115
A;Accession: I37519
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-362 <RES>
A;Cross-references: UNIPROT:P30483; EMBL:X61710; NID:g32182; PIDN:CAA43879.1; PID:g32183
A;Note: this allele is designated B*4501
C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: glycoprotein; heterodimer; transmembrane protein
F;1-24/Domain: signal sequence #status predicted <SIG>
F;220-285/Domain: immunoglobulin homology <IMM>
F;110/Binding site: carbohydrate (Asn) (covalent) #status predicted

  Query Match             7.2%;  Score 89;  DB 2;  Length 362;
  Best Local Similarity   21.3%;  Pred. No. 2.2;
  Matches   50;  Conservative   37;  Mismatches   88;  Indels   60;  Gaps   10;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              :| ||:  |::                  : :||   |  | :||| | ||
Db        154 LSSWTAADTAAQ-----------------ITQRKWEAARVAEQDRAYLEGLC------- 188

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPD-----CWKLSQYPCLQ 115
                    :  || |:     |  : ||  |   :|                || |  ||  :
Db        189 ------VESLRRYL-----ENGKETLQRADPPKTHVTHHPISDHEATLRCWALGFYPA-E 236

Qy        116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCY 175
              : :      ||      |::|  :  :    |   : |::  ::|     |      | ::|:
Db        237 ITLTWQRDGED----QTQDTELVETR----PAGDRTFQKWAAVVVPSGEE----QRYTCH 284

Qy        176 SDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYL-SLLCER 229
                ||  | : |    ||          |   :  |:|::|:| :   : :::| |
Db        285 VQHEGLPKPLTLRWEPSSQSTI-----PIVGIVAGLAVLAVVVIGAVVATVMCRR 334


RESULT 7
I61861
MHC HLA-B44.2 chain - human
C;Species: Homo sapiens (man)
C;Date: 02-Jul-1996 #sequence_revision 02-Jul-1996 #text_change 09-Jul-2004
C;Accession: I61861
R;Parham, P.; Lawlor, D.A.; Lomen, C.E.; Ennis, P.D.
J. Immunol. 142, 3937-3950, 1989
A;Title: Diversity and diversification of HLA-A,B,C alleles.
A;Reference number: I36956; MUID:89235215; PMID:2715640
A;Accession: I61861
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-362 <RES>
A;Cross-references: UNIPROT:P30481; GB:M24038; NID:g187811; PIDN:AAA59663.1; PID:g386900
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             7.1%;  Score 88;  DB 2;  Length 362;
  Best Local Similarity   21.3%;  Pred. No. 2.7;
  Matches   50;  Conservative   37;  Mismatches   88;  Indels   60;  Gaps   10;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              :| ||:  |::                  : :||   |  | :||| | ||
Db        154 LSSWTAADTAAQ-----------------ITQRKWEAARVAEQDRAYLEGLC------- 188

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPD-----CWKLSQYPCLQ 115
                    :  || |:     |  : ||  |   :|                || |  ||  :
Db        189 ------VESLRRYL-----ENGKETLQRADPPKTHVTHHPISDHEVTLRCWALGFYPA-E 236

Qy        116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCY 175
              : :      ||      |::|  :  :    |   : |::  ::|     |      | ::|:
Db        237 ITLTWQRDGED----QTQDTELVETR----PAGDRTFQKWAAVVVPSGEE----QRYTCH 284

Qy        176 SDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYL-SLLCER 229
                ||  | : |    ||          |   :  |:|::|:| :   : :::| |
Db        285 VQHEGLPKPLTLRWEPSSQSTV-----PIVGIVAGLAVLAVVVIGAVVAAVMCRR 334


RESULT 8
T18531
tractin - medicinal leech
C;Species: Hirudo medicinalis (medicinal leech)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T18531
R;Huang, Y.; Jellies, J.; Johansen, K.M.; Johansen, J.
J. Cell Biol. 138, 143-157, 1997
A;Title: Differential glycosylation of Tractin and LeechCAM, two novel Ig-superfamily mem
A;Reference number: Z18951; MUID:97362067; PMID:9214388
A;Accession: T18531
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-1880 <HUA>
A;Cross-references: UNIPROT:O18465; EMBL:U92813; NID:g2275259; PID:g2275260; PIDN:AAC4765

  Query Match             7.1%;  Score 87.5;  DB 2;  Length 1880;
  Best Local Similarity   22.0%;  Pred. No. 19;
  Matches   42;  Conservative   24;  Mismatches   64;  Indels   61;  Gaps    8;

Qy         21 IYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRS------YM 74
              ::|  :| : |:| :      |  ||:                    |||  :      |
Db         64 VFQWFKDGEPLEKSEAERPFK-DEDQGT-----------------ITLYNNELKDEGYY 104

Qy         75 QSV-----WTEESQCTLLNASITETF--------------NCSFSCGPDCWKLSQYPCL 114
              | :      |  |  |||  :: |:|                | :  | ||       ||
Db        105 QCIVKNKYGTAASVKTLLKMAVQESFPTVKEPQIVNVRVGDNLTLRCNPP----KSYPTP 160

Qy        115 QVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSC 174
               ||       | |||     | |:: |             ::| :    ||: |: |:  :: |
Db        161 DVYWGTVKKGAKLL--PLENTMRYN----------LDYEGNFHFANVMEEDHREGAYYLC 208

Qy        175 YSDPEGNQKSV 185
                |      : ||
```

```
Db        209 ISHNNAMRSSV 219


RESULT 9
F90206
histidinol dehydrogenase (HDH) (hisD) [imported] - Sulfolobus solfataricus
C;Species: Sulfolobus solfataricus
C;Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 16-Aug-2004
C;Accession: F90206
R;She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
 Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, P
arrett, R.A.; Ragan, M.A.; Sensen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A;Description: Sulfolobus solfataricus complete genome.
A;Reference number: A99139
A;Accession: F90206
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-398 <KUR>
A;Cross-references: UNIPROT:O33775; GB:AE006641; NID:g13813763; PIDN:AAK40909.1; GSPDB:G
C;Genetics:
A;Gene: hisD
C;Superfamily: Histidinol dehydrogenase; histidinol dehydrogenase homology

  Query Match             7.0%;  Score 87;  DB 2;  Length 398;
  Best Local Similarity   22.8%;  Pred. No. 3.7;
  Matches   34;  Conservative   25;  Mismatches   50;  Indels   40;  Gaps    7;

Qy        102 GPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNV 161
              |||             |: |.|: :: |:   || || ::|  || |  || :|:: : |
Db        248 GPD-----------TYIVLLSNDDE-LIRRVEEKIKNDKKIYYIIKT-KNLDEAIEIANK 294

Qy        162 VMENFRKYQHFSCYSDPE--------------GNQKSVILTKLYSSNVLFHSLFWPTCM 206
              :       :| | |                 ||    |: :   | :  :  |
Db        295 IAP-----EHLSLYVKDAYTLMDKIVNAGAISLGNTPPAIIDYVAGPNHILPTNGW--AK 347

Qy        207 MAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              : ||: :   :| | | :     :: ||:
Db        348 IRGGITVYDFIKPTMYAN-----VRDINK 371


RESULT 10
G87793
protein C27A12.7 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: G87793
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biolog
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_ele
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: G87793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-497 <STO>
A;Cross-references: UNIPROT:O01964; GB:chr_I; PIDN:AAB93644.1; PID:g2105479; GSPDB:GN000
C;Genetics:
A;Gene: C27A12.7
A;Map position: 1

  Query Match             7.0%;  Score 87;  DB 2;  Length 497;
  Best Local Similarity   19.4%;  Pred. No. 4.7;
  Matches   43;  Conservative   36;  Mismatches   87;  Indels   56;  Gaps    8;

Qy          5 TSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMY-- 62
              ||   :|  : |:|     :: |:|||:     |      |   :| :   || |:::
Db         37 TSDNDTSYAKEDKKSE--NEVLDNDLLEAEMNTTI----ADVQAVLQVDPGVCRILLHKY 90

Qy         63 -------------------FLLGITLLRSYMQSVWTEESQCTLLNASITET--FNCSFSC 101
                               ||:   ::    : :   :::| :   |: |    :|:
Db         91 KWNKESLLERLYEHPDTIAFLIDAQVIPRQQEVIPAGDAECDIC-CSMDELSGLSCNHRA 149

Qy        102 GPDCWKL-----------SQYPCLQVYVNLTSSGEKLLLYHTEET-------------IK 137
              :||:              |:  |:      |    ||:| |  : |             |:
Db        150 CAECWQAYLTNKIVSDAQSEIECMAPNCKLLIEDEKVLAYIKDPTIIAKYRKMMVASYIE 209

Qy        138 INQKCSYIP--KCGKNFEESMSLVNVVMENFRKYQHFSCYSD 177
              ||    : |   ||:  : |      :|:         |||  |
Db        210 INALLKWCPGVDCGRTVKVSHGEPRLVVCTCGSRFCFSCGQD 251


RESULT 11
B36284
prolactin-like protein II, placental - bovine
C;Species: Bos primigenius taurus (cattle)
C;Date: 18-Jan-1991 #sequence_revision 18-Jan-1991 #text_change 09-Jul-2004
C;Accession: B36284
R;Yamakawa, M.; Tanaka, M.; Koyama, M.; Kagesato, Y.; Watahiki, M.; Yamamoto, M.; Nakashi
J. Biol. Chem. 265, 8915-8920, 1990
A;Title: Expression of new members of the prolactin growth hormone gene family in bovine
A;Reference number: A36284; MUID:90256825; PMID:2341410
A;Accession: B36284
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-238 <YAM>
A;Cross-references: UNIPROT:P19159; GB:M33269; GB:J05458; NID:g163630; PIDN:AAA30740.1; P
C;Superfamily: prolactin

  Query Match             6.9%;  Score 86;  DB 2;  Length 238;
  Best Local Similarity   24.3%;  Pred. No. 2.5;
  Matches   36;  Conservative   19;  Mismatches   59;  Indels   34;  Gaps    7;

Qy         72 SYMQSVWT---EESQCTLL-----NASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSS 123
              |:    ||       | ||      |  : :  :|  ||||| :   |  : |::|  |
Db          6 SFRGHQWTYNPVRGSCLLLLLVVSNLLLCQGISCP-SCGPDMFVSLQKSLIDVFINAASL 64

Qy        124 GEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEGNQK 183
                 :|   ||  |:           |:|  :   :   |  |  | : :  ||   |
Db         65 SHD---FHNLSTIMFNE----------FDEKYAQGKLYYINATKSCHTNSFHTPEERDK 110

Qy        184 SV----------ILTKLYS-SNVLFHSL 200
              :           |  ||| :| |:: |
Db        111 AQQMNNEDLSKWTLVLLYSWNNPLYYLL 138


RESULT 12
F87793
protein C27A12.6 [imported] - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: F87793
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode C. elegans: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/C_elegans/ and www_sanger.ac.uk/Projects/C_eleg
A;Note: published errata appeared in Science 283, 35, 1999; Science 283, 2103, 1999; and
A;Accession: F87793
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-491 <STO>
A;Cross-references: UNIPROT:O01963; GB:chr_I; PIDN:AAB93643.1; PID:g2105478; GSPDB:GN000
C;Genetics:
A;Gene: C27A12.6
A;Map position: 1

  Query Match             6.9%;  Score 85.5;  DB 2;  Length 491;
  Best Local Similarity   18.5%;  Pred. No. 6.3;
  Matches   36;  Conservative   37;  Mismatches   57;  Indels   65;  Gaps    9;

Qy         14 RHDEKRNIY-------QKIRDHDLL--DKRKTVTALKAGEDRAILLGLAMMVCSIMMY-- 62
              |||:  : |        :: ||| |  : :| :: ::|      :| :    || |:::
Db         32 RHDQSASDYLNKKDKDNEVLDHDSLEAEMKKAISEVEA------VLQVKTGVCRILLHKY 85
```

```
Qy          63 ------------------FLLGITLLRSYMQSVWTEESQCTLLNASITET--FNCSFSC 101
                                 ||:  ::    : :   :::| :   |: |    :|:
Db          86 KWNKESLLERFYEHPDTIAFLIDAQVIPRQQEVIPAGDAECDIC-CSMDELSGLSCNHRA 144

Qy         102 GPDCWKL-----------SQYPCLQVYVNLTSSGEKLLLYHTEET------------IK 137
                 :||:            |:  |:      |    ||:| | :: |            ::
Db         145 CAECWQAYLTNKIVSDAQSEIECMAPNCKLLIEDEKVLSYISDPTMVSKYRKLMVASYVE 204

Qy         138 INQKCSYIP--KCGK 150
               ||    : |   |||
Db         205 INCLLRWCPGIDCGK 219


RESULT 13
S24451
hypothetical protein - phage SPP1
C;Species: phage SPP1
C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004
C;Accession: S24451; T42263
R;Chai, S.; Bravo, A.; Lueder, G.; Nedlin, A.; Trautner, T.A.; Alonso, J.C.
J. Mol. Biol. 224, 87-102, 1992
A;Title: Molecular analysis of the Bacillus subtilis bacteriophage SPP1 region encompass
A;Reference number: S24450; MUID:92194332; PMID:1548711
A;Accession: S24451
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-422 <CHA>
A;Cross-references: UNIPROT:P54308; EMBL:X56064; NID:g15464; PIDN:CAA39537.1; PID:g15466
R;Alonso, J.C.; Luder, G.; Stiege, A.C.; Chai, S.; Weise, F.; Trautner, T.A.
Gene 204, 201-212, 1997
A;Title: The complete nucleotide sequence and functional organization of Bacillus subtil
A;Reference number: Z22137; MUID:98094274; PMID:9434185
A;Accession: T42263
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-422 <ALO>
A;Cross-references: EMBL:X97918; PIDN:CAA66573.1

  Query Match             6.8%;  Score 84.5;  DB 2;  Length 422;
  Best Local Similarity   23.1%;  Pred. No. 6.6;
  Matches   48;  Conservative   29;  Mismatches   90;  Indels   41;  Gaps    9;

Qy          17 EKRNIYQKIRDHDLLDKRKTVTA-------LKAGEDRAILLGLAMMVCSIMMYFLLGITL 69
                  :|  : :|    |  |:  :|| |       || |    |    :|| :  :||   :   :
Db           2 KKVRLSEKFTPH-FLEVWRTVKAAQHLKYVLKGGRGSAKSTHIAMWIILLMMMMPITFLV 60

Qy          70 LRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLL 129
                  :|    :|  |:|    |  :|          |   ||:|: |    |:      |  ::
Db          61 IRRVYNTV--EQSVFEQLKEAID-----MLEVG-HLWKVSKSPLRLTYI---PRGNSIIF 109

Qy         130 YHTEETIKINQ-KCSYIPKCGKNFEE------------SMSLVNVVMENFRKYQHFSCY 175
                  ::  ||   | |  |  |   ||             |::   :    :|  |  |
Db         110 RGGDDVQKIKSIKASKFPVAGMWIEELAEFKTEEEVSVIEKSVLRAELPPGCRYIFFYSY 169

Qy         176 SDPEGNQKSVILTKLYSSNVLFHSLFWP 203
               : |:  |  |          | :|:| | |
Db         170 NPPKRKQSWV--------NKVFNSSFLP 189


RESULT 14
C35997
MHC class I histocompatibility antigen HLA-B37 alpha chain precursor - human
C;Species: Homo sapiens (man)
C;Date: 16-Nov-1990 #sequence_revision 13-Jan-1993 #text_change 09-Jul-2004
C;Accession: C35997
R;Ennis, P.D.; Zemmour, J.; Salter, R.D.; Parham, P.
Proc. Natl. Acad. Sci. U.S.A. 87, 2833-2837, 1990
A;Title: Rapid cloning of HLA-A,B cDNA by using the polymerase chain reaction: frequency
A;Reference number: A35997; MUID:90207291; PMID:2320591
A;Accession: C35997
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-362 <ENN>
A;Cross-references: UNIPROT:P18463; GB:M32320; NID:g187792; PIDN:AAA36233.1; PID:g307224
C;Genetics:
A;Gene: GDB:HLA-B
A;Cross-references: GDB:120048; OMIM:142830
A;Map position: 6p21.3-6p21.3
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
C;Keywords: transmembrane protein
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             6.8%;  Score 84;  DB 2;  Length 362;
  Best Local Similarity   21.3%;  Pred. No. 6.2;
  Matches   50;  Conservative   37;  Mismatches   88;  Indels   60;  Gaps   11;

Qy           1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
                 :| ||:  |::                    : :||   |  | :||| | |     |
Db         154 LSSWTAADTAAQ-----------------ITQRKWEAARVAEQDRAYLEG----TC--- 188

Qy          61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPD-----CWKLSQYPCLQ 115
                    :  || |:     |  : ||  |   :|                 ||  |  ||  :
Db         189 ------VEWLRRYL-----ENGKETLQRADPPKTHVTHHPISDHEATLRCWALGFYPA-E 236

Qy         116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCY 175
               : :     ||       |::|  :  :    |   : |::  ::|     |     | ::|:
Db         237 ITLTWQRDGED----QTQDTELVETR----PAGDRTFQKWAAVVVPSGEE----QRYTCH 284

Qy         176 SDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYL-SLLCER 229
                  ||  | : |    ||          |   :  |:|::|:|  :    : :::| |
Db         285 VQHEGLPKPLTLRWEPSSQSTI-----PIVGIVAGLAVLAVVVIGAVVATVMCRR 334


RESULT 15
I38421
gene HLA B-1519 protein - human
C;Species: Homo sapiens (man)
C;Date: 21-Feb-1997 #sequence_revision 21-Feb-1997 #text_change 09-Jul-2004
C;Accession: I38421
R;Hildebrand, W.H.; Domena, J.D.; Shen, S.Y.; Lau, M.; Terasaki, P.I.; Bunce, M.; Marsh,
Tissue Antigens 43, 209-218, 1994
A;Title: HLA-B15: a widespread and diverse family of HLA-B alleles.
A;Reference number: I38421; MUID:94367483; PMID:7521976
A;Accession: I38421
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: mRNA
A;Residues: 1-362 <RES>
A;Cross-references: UNIPROT:P30464; EMBL:U03027; NID:g413769; PIDN:AAA18902.1; PID:g4137
C;Genetics:
A;Gene: HLA-B-1519
C;Superfamily: class I histocompatibility antigen; immunoglobulin homology
F;220-285/Domain: immunoglobulin homology <IMM>

  Query Match             6.7%;  Score 83;  DB 2;  Length 362;
  Best Local Similarity   20.9%;  Pred. No. 7.6;
  Matches   49;  Conservative   39;  Mismatches   87;  Indels   60;  Gaps   10;

Qy           1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
                 :| ||:  |::                    : :||   | :| : || | ||
Db         154 LSSWTAADTAAQ-----------------ITQRKWEAAREAEQWRAYLEGLC------- 188

Qy          61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPD-----CWKLSQYPCLQ 115
                    :  || |:     |  : ||  |   :|                 ||  |  ||  :
Db         189 ------VDGLRRYL-----ENGKETLQRADPPKTHVTHHPISDHEATLRCWALGFYPA-E 236

Qy         116 VYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCY 175
               : :     ||       |::|  :  :    |   : |::  ::| :  |     | ::|:
Db         237 ITLTWQRDGED----QTQDTELVETR----PAGDRTFQKWAAVVVLSGEE----QRYTCH 284

Qy         176 SDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYL-SLLCER 229
                  ||  | : |    ||          |   :  |:|::|:|  :    : :::| |
Db         285 VQHEGLPKPLTLRWEPSSQSTI-----PIVGIVAGLAVLAVVVIGAVVATVMCRR 334


Search completed: November  6, 2004, 23:32:42
Job time : 20 secs
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GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 6, 2004, 23:22:16 ; Search time 65 Seconds
(without alignments)
1296.944 Million cell updates/sec

Title: US-09-914-053A-5
Perfect score: 1241
Sequence: 1 MSIWTSGRTSSSYRHDEKRN.....MVKLTQYLSLLCERIQRINR 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2002273 seqs, 358729299 residues

Total number of hits satisfying chosen parameters: 2002273

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : A_Geneseq_23Sep04:*
1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
4: geneseqp2001s:*
5: geneseqp2002s:*
6: geneseqp2003as:*
7: geneseqp2003bs:*
8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1241	100.0	235	3	AAB08820	Aab08820 Amino aci
2	1235	99.5	235	4	AAB35301	Aab35301 Human cal
3	1228	99.0	235	3	AAY70466	Aay70466 Human mem
4	971	78.2	182	6	ADA56755	Ada56755 Human sec
5	971	78.2	182	6	ADA40606	Ada40606 Human sec
6	971	78.2	183	3	AAY91460	Aay91460 Human sec
7	971	78.2	183	8	ADL71532	Adl71532 Novel hum
8	886	71.4	165	3	AAY91601	Aay91601 Human sec
9	886	71.4	165	8	ADL71677	Adl71677 Novel hum
10	484	39.0	137	4	ABB12189	Abb12189 Human K c
11	478.5	38.6	277	4	AAB35302	Aab35302 Human cal
12	477.5	38.5	277	4	AAM78995	Aam78995 Human pro
13	477.5	38.5	301	4	ABB11970	Abb11970 Human Ca-
14	477.5	38.5	301	4	AAM79979	Aam79979 Human pro
15	475	38.3	275	4	AAB35304	Aab35304 Human cal
16	474	38.2	257	3	AAB08818	Aab08818 Amino aci
17	474	38.2	257	4	AAB35303	Aab35303 Human cal
18	474	38.2	279	4	AAB35305	Aab35305 Human cal
19	435.5	35.1	220	2	AAY34131	Aay34131 Human pot
20	421	33.9	190	7	ADE54752	Ade54752 Human Pro
21	421	33.9	191	2	AAR85306	Aar85306 Human cal
22	421	33.9	191	5	ABP53982	Abp53982 Human Max
23	421	33.9	191	5	ABJ10903	Abj10903 K+beta M6
24	421	33.9	191	5	ABP51818	Abp51818 Human Max
25	421	33.9	191	5	ADJ33391	Adj33391 Human Max
26	421	33.9	191	7	ADD14147	Add14147 Human src
27	418	33.7	191	7	ADE54750	Ade54750 Rat Prote
28	382	30.8	191	2	AAR85305	Aar85305 Bovine ca
29	352	28.4	202	4	AAM96297	Aam96297 Human rep
30	318	25.6	218	3	AAB41606	Aab41606 Human ORF
31	317	25.5	210	7	ADJ69109	Adj69109 Human hea
32	316	25.5	210	2	AAY21839	Aay21839 Human cal
33	316	25.5	210	3	AAY77561	Aay77561 Human pot
34	316	25.5	210	3	AAB08819	Aab08819 Amino aci
35	177	14.3	85	3	AAG03607	Aag03607 Human sec
36	125	10.1	928	4	ABG13226	Abg13226 Novel hum
37	125	10.1	928	4	ABG13406	Abg13406 Novel hum
38	125	10.1	928	4	ABG18125	Abg18125 Novel hum
39	120.5	9.7	185	2	AAY07968	Aay07968 Human sec
40	93.5	7.5	496	8	ADQ08798	Adq08798 Ciona int
41	92	7.4	897	6	ABU40481	Abu40481 Protein e
42	92	7.4	897	7	ADF03964	Adf03964 Bacterial
43	91.5	7.4	448	4	ABB67183	Abb67183 Drosophil
44	91	7.3	347	4	AAM41242	Aam41242 Human pol
45	91	7.3	807	8	ADJ66497	Adj66497 KIAA0792

ALIGNMENTS

RESULT 1
AAB08820
ID AAB08820 standard; protein; 235 AA.
XX
AC AAB08820;
XX
DT 02-JAN-2001 (first entry)
XX
DE Amino acid sequence of a human BK beta-4 polypeptide.
XX
KW Human; BK beta-2; beta subunit; Slo potassium channel; BK beta-3;
KW BK beta-4; ion flux; migraine; hearing; vision problem; seizure; stroke;
KW asthma; cell proliferation; hormone secretion; cancer; viral infection.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Misc-difference 230
FT /note= "encoded by CA"
XX
PN WO200050444-A1.
XX
PD 31-AUG-2000.
XX
PF 22-FEB-2000; 2000WO-US004441.
XX
PR 23-FEB-1999; 99US-0121224P.
PR 03-NOV-1999; 99US-0163367P.
XX
PA (ICAG-) ICAGEN INC.
XX
PI Jegla TJ, Wickenden A, Liu Y;
XX
DR WPI; 2000-533179/48.
DR N-PSDB; AAA75011.
XX
PT Isolated beta subunit polynucleotides and polypeptides of Slo potassium
PT channels are used to determine the effects of compounds on ion flux
PT through a potassium channel and in computer modelling systems.
XX
PS Claim 17; Page 79; 84pp; English.
XX
CC The present sequence represents a human BK beta-4 polypeptide. The
CC polypeptide is a beta subunit of a Slo potassium channel. The
CC specification also describes BK beta-3 and BK beta-2 polypeptides. BK
CC beta subunits are auxiliary subunits or monomers of Slo potassium
CC channels. The polypeptides, when expressed in cells and cell membranes,
CC are used to determine the effects of compounds on ion flux through a

CC potassium channel. The compounds identified may be useful as therapeutic
CC agents e.g. modulators that target specific Slo channels are useful for
CC treating migraines, hearing and vision problems, seizures, stroke,
CC asthma, cell proliferation and hormone secretion. The computer generated
CC 3-dimensional structures of BK beta 2, BK beta 3 or BK beta 4 are used to
CC identify ligands that bind to the beta subunit. The characterized BK beta
CC subunits are used to determine how Slo potassium channels function in
CC different environments and how they respond to different activation
CC mechanisms. The polynucleotides are used to transfect cells in vivo and
CC in vitro to mitigate effects of absent, partial inactivation or abnormal
CC expression of the BK beta subunit gene e.g. to correct genetic defects,
CC cancer and viral infection
XX
SQ Sequence 235 AA;

Query Match 100.0%; Score 1241; DB 3; Length 235;
Best Local Similarity 100.0%; Pred. No. 3.9e-129;
Matches 235; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
Db 1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy 61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
Db 61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120

Qy 121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
Db 121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180

Qy 181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
Db 181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235

RESULT 2
AAB35301
ID AAB35301 standard; protein; 235 AA.
XX
AC AAB35301;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human calcium sensitive potassium channel beta2 subunit.
XX
KW Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW irritable bowel syndrome; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200105828-A1.
XX
PD 25-JAN-2001.
XX
PF 18-JUL-2000; 2000WO-US019585.
XX
PR 20-JUL-1999; 99US-0144764P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Uebele V, Swanson R, Liu Y, Lagrutta A;
XX
DR WPI; 2001-159514/16.
DR N-PSDB; AAF27991.
XX
PT Novel human calcium sensitive potassium channel subunits for identifying
PT inhibitors and agonists of the potassium channel for use in treating
PT conditions such as asthma, hypertension, memory disorders, depression.
XX
PS Claim 9; Fig 1B; 89pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC and beta3d subunits. These can be used to identify inhibitors and
CC activators of the channels, which can be used in the treatment of
CC conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC incontinence, migraine and irritable bowel syndrome. The coding sequences
CC are found at human chromosome 3q23-ter. The present sequence is the beta2
CC subunit
XX
SQ Sequence 235 AA;

Query Match 99.5%; Score 1235; DB 4; Length 235;
Best Local Similarity 99.6%; Pred. No. 1.8e-128;
Matches 234; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

Qy 1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
Db 1 MFIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy 61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
Db 61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120

Qy 121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
Db 121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180

Qy 181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
Db 181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235

RESULT 3
AAY70466
ID AAY70466 standard; protein; 235 AA.
XX
AC AAY70466;
XX
DT 21-JUN-2000 (first entry)
XX
DE Human membrane channel protein-16 (MECHP-16).
XX
KW Membrane channel protein-16; MECHP-16; diagnosis; treatment; lymphoma;
KW cell proliferative disorder; bursitis; atherosclerosis; cancer; sarcoma;
KW inflammatory disorder; AIDS; Addison's disease; cystic fibrosis; asthma;
KW diabetes mellitus; osmoregulatory disorder; diarrhoea; renal failure;
KW muscular disorder; myocarditis; Duchenne's muscular dystrophy; nootropic;
KW cardiovascular disorder; hypertension; bronchitis; vasculitis; cardiant;
KW neurological disorder; Alzheimer's disease; Parkinson's disease; human;
KW Huntington's disease; antiarteriosclerotic; hepatotropic; cytostatic;
KW anti-HIV; antianaemic; neuroprotective; immunomodulator; antidiabetic;
KW hypotensive; vasotropic; antiasthmatic; antiinflammatory; antidepressant;
KW anticonvulsant; thrombolytic; antiParkinsonian; immunostimulant.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT Modified-site 6
FT /note= "Phosphorylation site"
FT Modified-site 12
FT /note= "Phosphorylation site"
FT Modified-site 36
FT /note= "Phosphorylation site"
FT Domain 48. .68
FT /label= Transmembrane_domain
FT Modified-site 88
FT /note= "Glycosylation site"
FT Modified-site 90
FT /note= "Phosphorylation site"
FT Modified-site 96
FT /note= "Glycosylation site"

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FT   Modified-site   119
FT                   /note= "Glycosylation site"
FT   Modified-site   122
FT                   /note= "Phosphorylation site"
FT   Modified-site   135
FT                   /note= "Phosphorylation site"
FT   Modified-site   176
FT                   /note= "Phosphorylation site"
XX
PN   WO200012711-A2.
XX
PD   09-MAR-2000.
XX
PF   02-SEP-1999;   99WO-US020468.
XX
PR   02-SEP-1998;   98US-0155226P.
PR   12-NOV-1998;   98US-00191283.
PR   09-DEC-1998;   98US-0155225P.
PR   26-JAN-1999;   99US-0155211P.
PR   10-FEB-1999;   99US-0155263P.
XX
PA   (INCY-) INCYTE PHARM INC.
XX
PI   Au-Young J,  Bandman O,  Tang YT,  Reddy R,  Hillman JL,  Yue H;
PI   Lal P,  Corley NC,  Guegler KJ,  Gorgone G,  Baughn MR,  Azimzai Y;
XX
DR   WPI; 2000-256643/22.
DR   N-PSDB; AAZ51632.
XX
PT   Novel human membrane channel protein and polynucleotide useful for
PT   diagnosing and treating cell proliferative, inflammatory, secretory,
PT   osmoregulatory, muscular, cardiovascular and neurological disorders.
XX
PS   Claim 1; Page 115; 140pp; English.
XX
CC   The present sequence is the human membrane channel protein-16 (MECHP-16),
CC   which is expressed in nervous tissues. Anti-MECHP antibodies can be used
CC   as therapeutic antagonists and reagents for diagnosis and monitoring
CC   diseases. MECHP cDNA can be used for diagnosis of MECHP-related diseases
CC   and gene mapping. MECHP can be used for treatment of cell proliferative
CC   disorders such as bursitis and atherosclerosis, cancers like lymphoma and
CC   sarcoma, inflammatory disorders like AIDS and Addison's disease,
CC   transport/secretory disorders like cystic fibrosis and diabetes mellitus,
CC   osmoregulatory disorders like diarrhoea and renal failure, muscular
CC   disorders like myocarditis and Duchenne's muscular dystrophy,
CC   cardiovascular disorders like hypertension and vasculitis, congenital
CC   lung anomalies like bronchitis and asthma and neurological disorders like
CC   Alzheimer's disease, Parkinson's disease and Huntington's disease
XX
SQ   Sequence 235 AA;

  Query Match             99.0%;  Score 1228;  DB 3;  Length 235;
  Best Local Similarity   99.1%;  Pred. No. 1.1e-127;
  Matches  233;  Conservative    0;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||
Db         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCPQVYVNL 120

Qy        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235

RESULT 4
ADA56755
ID   ADA56755 standard; protein; 182 AA.
XX
AC   ADA56755;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein #37.
XX
KW   immunosuppressive; antiinflammatory; antiasthmatic; antiallergic;
KW   cytostatic; cerebroprotective; neuroprotective; nootropic;
KW   cardiovascular; antiarteriosclerotic; gene therapy;
KW   human secreted protein; immune disorder; inflammation;
KW   respiratory disorder; cancer; CNS disorder; neurodegenerative disorders;
KW   inflammatory bowel disease; nephritis; Crohn's disease; asthma; allergy;
KW   multiple sclerosis; ischaemic brain injury; Parkinson's disease;
KW   Alzheimer's disease; atherosclerosis; myocarditis; chromosome mapping;
KW   triple helix formation; antisense gene therapy; forensic biology.
XX
OS   Homo sapiens.
XX
PN   WO2002102994-A2.
XX
PD   27-DEC-2002.
XX
PF   19-MAR-2002; 2002WO-US008278.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-167512/16.
DR   N-PSDB; ADA55858.
XX
PT   New human secreted polypeptides and polynucleotides, useful for
PT   diagnosing, treating or preventing e.g. immune disorders, inflammatory
PT   conditions, respiratory disorders, cancers, CNS disorders, or
PT   neurodegenerative disorders.
XX
PS   Claim 13; SEQ ID NO 944; 1754pp; English.
XX
CC   The invention relates to 592 new human secreted polypeptides useful for
CC   diagnosing, treating or preventing e.g. immune disorders, inflammatory
CC   conditions, respiratory disorders, cancers, CNS disorders, or
CC   neurodegenerative disorders, or polypeptides comprising an amino acid
CC   sequence at least 95% identical to the new sequences. The polypeptides,
CC   antibodies or antibody fragments that bind to the polypeptides, nucleic
CC   acids encoding the polypeptides, agonists or antagonists that binds to
CC   the polypeptide, are useful in preparing diagnostic or pharmaceutical
CC   compositions for diagnosing, treating or preventing an e.g. immune
CC   disorders, inflammatory conditions (e.g. inflammatory bowel disease,
CC   nephritis or Crohn's disease), respiratory disorders (e.g. asthma and
CC   allergy), cancers (e.g. gastric, ovarian or lung cancer), CNS disorders
CC   (e.g. multiple sclerosis or ischaemic brain injury), neurodegenerative
CC   disorders (e.g. Parkinson's disease or Alzheimer's disease), and
CC   cardiovascular disorders (e.g. atherosclerosis or myocarditis). The
CC   polynucleotides are useful for chromosome identification, chromosome
CC   mapping, for controlling gene expression through triple helix formation
CC   or antisense DNA or RNA, in gene therapy, for identifying individuals
CC   from minute biological samples, in forensic biology, and as hybridization
CC   probes. The polypeptides are useful for as molecular weight markers on
CC   sodium dodecyl sulfate-polyacrylamide gel electrophoresis (SDS-PAGE)
CC   gels, to raise antibodies, for testing biological activities, and for
CC   treating or preventing neural disorders, immune system disorders,
CC   muscular, reproductive, gastrointestinal, pulmonary, cardiovascular,
CC   renal, proliferative and/or cancerous diseases. This sequence corresponds
CC   to one of the polypeptide of the invention. Note: The sequence data for
CC   this patent did form part of the printed specification, but was obtained
CC   in electronic format directly from WIPO at
```

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CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 182 AA;

  Query Match             78.2%;  Score 971;  DB 6;  Length 182;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-99;
  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 60

Qy        114 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 120

Qy        174 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 180

Qy        234 NR 235
              ||
Db        181 NR 182


RESULT 5
ADA40606
ID   ADA40606 standard; protein; 182 AA.
XX
AC   ADA40606;
XX
DT   20-NOV-2003  (first entry)
XX
DE   Human secreted protein.
XX
KW   Human; secreted protein; cancer; hyperproliferative disorder;
KW   rheumatoid arthritis; autoimmune disorder; haematopoietic disorder;
KW   anaemia; allergic reaction; asthma; cardiovascular disorder;
KW   wound healing; cytostatic; immunosuppressive; nootropic; neuroprotective;
KW   antiviral; antiallergic; hepatotropic; antidiabetic; antiinflammatory;
KW   vulnerary; cardiant; gene therapy.
XX
OS   Homo sapiens.
XX
PN   WO2002102993-A2.
XX
PD   27-DEC-2002.
XX
PF   19-MAR-2002; 2002WO-US008123.
XX
PR   21-MAR-2001; 2001US-0277340P.
PR   19-JUL-2001; 2001US-0306171P.
PR   13-NOV-2001; 2001US-0331287P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Rosen CA,  Ruben SM;
XX
DR   WPI; 2003-175238/17.
XX
PT   New human secreted proteins and nucleic acid molecules, useful for
PT   preparing a diagnostic or pharmaceutical composition for diagnosing,
PT   preventing or treating cancer or other hyperproliferative disorder,
PT   asthma, allergies or AIDS.
XX
PS   Claim 1; SEQ ID NO 988; 3205pp; English.
XX
CC   The invention relates to novel genes ADA39629-ADA40565 and proteins
CC   ADA40566-ADA41501 for human secreted proteins, useful for preventing,
CC   treating or ameliorating medical conditions e.g. by protein or gene
CC   therapy. The polypeptides, nucleic acid molecules, antibodies or their
CC   fragments, and agonists or antagonists that bind to the polypeptide are
CC   useful for preparing a diagnostic or pharmaceutical composition for
CC   diagnosing or treating cancer or other hyperproliferative disorder. The
CC   polypeptides and nucleic acid molecules are also useful for detecting,
CC   preventing, diagnosing, prognosticating, treating or ameliorating cancer
CC   or other hyperproliferative disorders including neoplasms, autoimmune
CC   disorders (e.g. diabetes, rheumatoid arthritis, systemic lupus
CC   erythematosus, multiple sclerosis, autoimmune thyroiditis or haemolytic
CC   anaemia), haematopoietic or haematological disorders (e.g. anaemia,
CC   thrombocytopenia), allergic reactions including asthma or eczema,
CC   inflammatory disorders (e.g. ischaemia-reperfusion injury, inflammatory
CC   bowel disease or Crohn's disease), neurodegenerative disorders (e.g.
CC   Alzheimer's disease or Parkinson's disease), cardiovascular disorders
CC   (e.g. atherosclerosis, myocarditis), infectious diseases (bacterial,
CC   fungal or viral infections including HIV/AIDS), or wound healing and
CC   disorders of epithelial cell proliferation. The nucleic acids are also
CC   useful for chromosome identification, radiation hybrid mapping or long-
CC   range restriction mapping, as molecular weight markers, or as
CC   hybridization or diagnostic probes. The polypeptides and antibodies are
CC   useful for providing immunological probes for differential identification
CC   of the tissues immunohistochemistry assays. Note: The sequence data for
CC   this patent did not form part of the printed specification, but was
CC   obtained in electronic format directly from WIPO at
CC   ftp.wipo.int/pub/published_pct_sequences.
XX
SQ   Sequence 182 AA;

  Query Match             78.2%;  Score 971;  DB 6;  Length 182;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-99;
  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 60

Qy        114 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 120

Qy        174 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 180

Qy        234 NR 235
              ||
Db        181 NR 182


RESULT 6
AAY91460
ID   AAY91460 standard; protein; 183 AA.
XX
AC   AAY91460;
XX
DT   29-JUN-2000  (first entry)
XX
DE   Human secreted protein sequence encoded by gene 10 SEQ ID NO:133.
XX
KW   Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW   antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW   osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW   antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW   immune disease; inflammation; blood disorder; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200006698-A1.
XX
PD   10-FEB-2000.
XX
PF   29-JUL-1999;   99WO-US017130.
XX
PR   30-JUL-1998;   98US-0094657P.
PR   05-AUG-1998;   98US-0095486P.
PR   06-AUG-1998;   98US-0095454P.
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PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
XX
PA (HUMA-) HUMAN GENOME SCI INC.
XX
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan R, Moore PA, Shi Y;
PI Lafleur D, Wei Y, Ni J, Florence KA, Young PE, Brewer LA;
PI Soppet DR, Endress GA, Ebner R, Olsen HS, Mucenski M;
XX
DR WPI; 2000-195282/17.
DR N-PSDB; AAA26355.
XX
PT New isolated human genes and the secreted polypeptides they encode,
PT useful for diagnosis and treatment of e.g. cancers, neurological
PT disorders, immune diseases, inflammation or blood disorders.
XX
PS Claim 11; Page 463; 634pp; English.
XX
CC The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC proteins can have activities based on the tissues and cells they are
CC expressed in. Examples of the activities are: cytostatic;
CC immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC corresponding secreted proteins are useful for preventing, treating or
CC ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC pathological conditions can be diagnosed by determining the amount of the
CC proteins in a sample or by determining the presence of mutations in the
CC polynucleotides. Specific uses are described for each of the
CC polynucleotides, based on which tissues they are most highly expressed
CC in, and include developing products for the diagnosis or treatment of
CC cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC and foetal deficiencies, blood disorders, diseases of the immune system,
CC autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC reproductive disorders, gastrointestinal disorders, respiratory disorders
CC and metabolic disorders. The proteins or polynucleotides can also be used
CC as food additives or preservatives. The proteins are also useful for
CC identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC sequences used in the exemplification of the present invention
XX
SQ Sequence 183 AA;

Query Match 78.2%; Score 971; DB 3; Length 183;
Best Local Similarity 100.0%; Pred. No. 2.9e-99;
Matches 182; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Qy          54 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 113
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db           1 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 60

Qy         114 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 173
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          61 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 120

Qy         174 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 233
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         121 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 180

Qy         234 NR 235
               ||
Db         181 NR 182
```

RESULT 7
ADL71532
ID ADL71532 standard; protein; 183 AA.
XX
AC ADL71532;
XX
DT 20-MAY-2004 (first entry)
XX
DE Novel human secreted protein seqid 136.
XX
KW antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KW anticonvulsant; antilipaemic; CNS; gynaecological; antiarthritic;
KW antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
KW immunosuppressive; antiallergic; cardiovascular; respiratory;
KW dermatological; antimicrobial; gastrointestinal; gene therapy;
KW neurodegenerative disease; behavioral disorder; inflammatory condition;
KW hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
KW Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW respiratory disorder; pulmonary disorder; connective tissue disorder;
KW skin disorder; CNS disorder; congenital disorder; infectious disorder;
KW gastrointestinal disorder; human; secreted protein.
XX
OS Homo sapiens.
XX
PN US2004034196-A1.
XX
PD 19-FEB-2004.
XX
PF 27-JAN-2003; 2003US-00351334.
XX
PR 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
PR 29-JUL-1999; 99WO-US017130.
PR 24-JAN-2000; 2000US-00489847.
PR 25-JAN-2002; 2002US-0350898P.
XX
PA (KOMA/) KOMATSOULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (WEIY/) WEI Y.
XX
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan DR, Moore PA, Shi Y;
PI Lafleur DW, Wei Y;
XX
DR WPI; 2004-180094/17.
DR N-PSDB; ADL71416.
XX
PT New human secreted nucleic acid, useful for diagnosing and treating
PT neurodegenerative, inflammatory, hyperproliferative, metabolic,
PT reproductive, cardiovascular, respiratory or immunological disorders or
PT diseases.
XX
PS Claim 11; SEQ ID NO 136; 234pp; English.
XX
CC The invention describes an isolated human nucleic acid molecule (I)
CC comprising a polynucleotide having a nucleotide sequence at least 95%
CC identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
CC the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
CC to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
CC epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
CC sequence included in ATCC Deposit No: Z, which is hybridisable to SEQ ID
CC NO: X, having a biological activity. The nucleic acids and polypeptides,
CC pharmaceutical formulations and kits are useful in diagnosing and
CC treating neurodegenerative diseases states, behavioral disorders,
CC inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
CC disease, Parkinson's diseases or Huntington's diseases), metabolic
CC disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
CC disorders, immunological disorders (e.g. arthritis, asthma or AIDS),

```
CC   endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
CC   or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
CC   cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
CC   conditions afflicting connective tissue, skin disorders, CNS disorders,
CC   congenital disorders, infectious disorders and gastrointestinal
CC   disorders. This is the amino acid sequence of a novel human secreted
CC   protein of the invention. Note: This sequence does not appear in the
CC   printed specification but is available in electronic format from the US
CC   patent office at ftp.seqdata.uspto.gov/seqdata.html?DocID=20040034196.
XX
SQ   Sequence 183 AA;

  Query Match             78.2%;  Score 971;  DB 8;  Length 183;
  Best Local Similarity   100.0%;  Pred. No. 2.9e-99;
  Matches  182;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         54 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 113
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPC 60

Qy        114 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 173
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 LQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFS 120

Qy        174 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 233
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 CYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRI 180

Qy        234 NR 235
              ||
Db        181 NR 182


RESULT 8
AAY91601
ID   AAY91601 standard; protein; 165 AA.
XX
AC   AAY91601;
XX
DT   29-JUN-2000  (first entry)
XX
DE   Human secreted protein sequence encoded by gene 10 SEQ ID NO:274.
XX
KW   Human; secreted protein; diagnosis; cytostatic; immunosuppressive;
KW   antiHIV; antiinflammatory; nootropic; neuroprotective; antiallergic;
KW   osteopathic; antiarthritic; antibacterial; antidiabetic; antiasthma;
KW   antipsoriatic; cardiant; gene therapy; cancer; neurological disorder;
KW   immune disease; inflammation; blood disorder; tumour.
XX
OS   Homo sapiens.
XX
PN   WO200006698-A1.
XX
PD   10-FEB-2000.
XX
PF   29-JUL-1999;   99WO-US017130.
XX
PR   30-JUL-1998;   98US-0094657P.
PR   05-AUG-1998;   98US-0095486P.
PR   06-AUG-1998;   98US-0095454P.
PR   06-AUG-1998;   98US-0095455P.
PR   12-AUG-1998;   98US-0096319P.
XX
PA   (HUMA-) HUMAN GENOME SCI INC.
XX
PI   Komatsoulis GA,  Rosen CA,  Ruben SM,  Duan R,  Moore PA,  Shi Y;
PI   Lafleur D,  Wei Y,  Ni J,  Florence KA,  Young PE,  Brewer LA;
PI   Soppet DR,  Endress GA,  Ebner R,  Olsen HS,  Mucenski M;
XX
DR   WPI; 2000-195282/17.
XX
PT   New isolated human genes and the secreted polypeptides they encode,
PT   useful for diagnosis and treatment of e.g. cancers, neurological
PT   disorders, immune diseases, inflammation or blood disorders.
XX
PS   Disclosure; Page 29; 634pp; English.
XX
CC   The polynucleotide sequences given in AAA26346 to AAA26458 encode the
CC   human secreted proteins given in AAY91451 to AAY91691. The human secreted
CC   proteins can have activities based on the tissues and cells they are
CC   expressed in. Examples of the activities are: cytostatic;
CC   immunosuppressive; antiHIV; antiinflammatory; nootropic; neuroprotective;
CC   antiallergic; osteopathic; antiarthritic; antibacterial; antidiabetic;
CC   antiasthma; antipsoriatic; and cardiant. The polynucleotides and their
CC   corresponding secreted proteins are useful for preventing, treating or
CC   ameliorating medical conditions, e.g. by protein or gene therapy. Also
CC   pathological conditions can be diagnosed by determining the amount of the
CC   proteins in a sample or by determining the presence of mutations in the
CC   polynucleotides. Specific uses are described for each of the
CC   polynucleotides, based on which tissues they are most highly expressed
CC   in, and include developing products for the diagnosis or treatment of
CC   cancer, tumours, neurodegenerative disorders, developmental abnormalities
CC   and foetal deficiencies, blood disorders, diseases of the immune system,
CC   autoimmune diseases, hepatic and renal disease, inflammation, allergies,
CC   Alzheimer's and behavioural disorders, schizophrenia, osteoporosis,
CC   arthritis, infections, AIDS, spinal cord injuries, transplant rejection,
CC   diabetes, asthma, sepsis, acne, psoriasis, cardiovascular disorders,
CC   reproductive disorders, gastrointestinal disorders, respiratory disorders
CC   and metabolic disorders. The proteins or polynucleotides can also be used
CC   as food additives or preservatives. The proteins are also useful for
CC   identifying their binding partners. AAA26337 to AAA26345 and AAY91450 are
CC   sequences used in the exemplification of the present invention
XX
SQ   Sequence 165 AA;

  Query Match             71.4%;  Score 886;  DB 3;  Length 165;
  Best Local Similarity   100.0%;  Pred. No. 7.1e-90;
  Matches  165;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy         71 RSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLY 130
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLY 60

Qy        131 HTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKL 190
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKL 120

Qy        191 YSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 165


RESULT 9
ADL71677
ID   ADL71677 standard; protein; 165 AA.
XX
AC   ADL71677;
XX
DT   20-MAY-2004  (first entry)
XX
DE   Novel human secreted protein fragment seqid 281.
XX
KW   antiinflammatory; neuroprotective; nootropic; antiparkinsonian;
KW   anticonvulsant; antilipaemic; CNS; gynaecological; antiarthritic;
KW   antiasthmatic; anti-HIV; virucide; endocrine; cytostatic;
KW   immunosuppressive; antiallergic; cardiovascular; respiratory;
KW   dermatological; antimicrobial; gastrointestinal; gene therapy;
KW   neurodegenerative disease; behavioral disorder; inflammatory condition;
KW   hyperproliferative disorder; Alzheimer's disease; Parkinson's disease;
KW   Huntington's disease; metabolic disorder; Tay-Sach's disease;
KW   Leash-Nyhan syndrome; reproductive disorder; immunological disorder;
KW   arthritis; asthma; AIDS; endocrine disorder; immune disorder;
KW   Hodgkin's lymphoma; haematopoietic disorder; muscular disorder;
KW   leukaemia; autoimmune disorder; allergy; cancer; cardiovascular disorder;
KW   respiratory disorder; pulmonary disorder; connective tissue disorder;
KW   skin disorder; CNS disorder; congenital disorder; infectious disorder;
```

KW gastrointestinal disorder; human; secreted protein.
XX
OS Homo sapiens.
XX
PN US2004034196-A1.
XX
PD 19-FEB-2004.
XX
PF 27-JAN-2003; 2003US-00351334.
XX
PR 30-JUL-1998; 98US-0094657P.
PR 05-AUG-1998; 98US-0095486P.
PR 06-AUG-1998; 98US-0095454P.
PR 06-AUG-1998; 98US-0095455P.
PR 12-AUG-1998; 98US-0096319P.
PR 29-JUL-1999; 99WO-US017130.
PR 24-JAN-2000; 2000US-00489847.
PR 25-JAN-2002; 2002US-0350898P.
XX
PA (KOMA/) KOMATSOULIS G A.
PA (ROSE/) ROSEN C A.
PA (RUBE/) RUBEN S M.
PA (DUAN/) DUAN D R.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (WEIY/) WEI Y.
XX
PI Komatsoulis GA, Rosen CA, Ruben SM, Duan DR, Moore PA, Shi Y;
PI Lafleur DW, Wei Y;
XX
DR WPI; 2004-180094/17.
XX
PT New human secreted nucleic acid, useful for diagnosing and treating
PT neurodegenerative, inflammatory, hyperproliferative, metabolic,
PT reproductive, cardiovascular, respiratory or immunological disorders or
PT diseases.
XX
PS Disclosure; SEQ ID NO 281; 234pp; English.
XX
CC The invention describes an isolated human nucleic acid molecule (I)
CC comprising a polynucleotide having a nucleotide sequence at least 95%
CC identical to: a sequence polynucleotide fragment of SEQ ID NO: X or of
CC the cDNA sequence included in ATCC Deposit No: Z, which is hybridisable
CC to SEQ ID NO: X; or a sequence encoding a polypeptide fragment, domain or
CC epitope of SEQ ID NO: Y or a polypeptide sequence encoded by the cDNA
CC sequence included in ATCC Deposit No: Z, which is hybridisable to SEQ ID
CC NO: X, having a biological activity. The nucleic acids and polypeptides,
CC pharmaceutical formulations and kits are useful in diagnosing and
CC treating neurodegenerative diseases states, behavioral disorders,
CC inflammatory conditions, hyperproliferative disorders (e.g. Alzheimer's
CC disease, Parkinson's diseases or Huntington's diseases), metabolic
CC disorders (e.g. Tay-Sach's disease or Leash-Nyhan syndrome), reproductive
CC disorders, immunological disorders (e.g. arthritis, asthma or AIDS),
CC endocrine and immune disorders (e.g. Hodgkin's lymphoma), haematopoietic
CC or muscular disorders (e.g. leukaemia), autoimmune disorders, allergy,
CC cancer, cardiovascular, respiratory or pulmonary disorders, disorders or
CC conditions afflicting connective tissue, skin disorders, CNS disorders,
CC congenital disorders, infectious disorders and gastrointestinal
CC disorders. This is the amino acid sequence of a novel human secreted
CC protein fragment of the invention. Note: This sequence does not appear in
CC the printed specification but is available in electronic format from the
CC US patent office at ftp.seqdata.uspto.gov/seqdata.html?DocID=20040034196.
XX
SQ Sequence 165 AA;

Query Match 71.4%; Score 886; DB 8; Length 165;
Best Local Similarity 100.0%; Pred. No. 7.1e-90;
Matches 165; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```
Qy         71 RSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLY 130
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 RSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLY 60

Qy        131 HTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKL 190
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 HTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKL 120

Qy        191 YSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
               |||||||||||||||||||||||||||||||||||||||||||||
Db        121 YSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 165
```

RESULT 10
ABB12189
ID ABB12189 standard; peptide; 137 AA.
XX
AC ABB12189;
XX
DT 11-JAN-2002 (first entry)
XX
DE Human K channel subunit homologue, SEQ ID NO:2559.
XX
KW Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW chronic inflammatory condition; proliferative retinopathy;
KW atherosclerosis; coronary heart disease; arterial ischaemia;
KW bone disorder; osteoporosis; vascular growth disorder;
KW tissue regeneration; wound healing; infection; immune disorder;
KW cell culture; drug screening; gene therapy; antiinflammatory;
KW antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW antifungal; vulnerary; antiulcer.
XX
OS Homo sapiens.
XX
PN WO200157188-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US003800.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT;
XX
DR WPI; 2001-457740/49.
DR N-PSDB; ABA09433.
XX
PT Human proteins and DNA encoding sequences useful for preventing, treating
PT or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT and cancer.
XX
PS Claim 20; Page 314; 1963pp; English.
XX
CC Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC invention also relates to vectors and recombinant host cells comprising a
CC nucleotide of the invention, methods of producing the novel polypeptides,
CC antibodies against the polypeptides, methods of detecting the nucleotides
CC or polypeptides in a sample, and methods of identifying compounds which
CC bind to polypeptides of the invention. Although novel, many of the
CC polypeptides of the invention have homology to known proteins, thereby
CC giving an insight into their probable biological activities, and hence
CC potential therapeutic applications. The polypeptides of the invention may
CC have various activities, including cytokine, cell proliferation or cell
CC differentiation activities; stem cell growth factor activity;
CC haematopoiesis regulatory activity; tissue growth activity;
CC immunomodulatory activity; activin- or inhibin-related activities;
CC chemotactic or chemokinetic activities; haemostatic, thrombotic or

CC thrombolytic activities; receptor or ligand activities; or may be
CC involved in oncogenesis, cancer cell proliferation or metastasis.
CC Depending on their biological activities, polypeptides and nucleotides of
CC the invention are useful for preventing, treating or ameliorating medical
CC conditions, e.g., by protein or gene therapy. Such conditions include
CC cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC proliferative retinopathy, atherosclerosis, coronary heart disease,
CC arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC vascular growth. Polypeptides involved with tissue regeneration and
CC repair (or nucleic acids encoding them) may be used to promote wound
CC healing (e.g., of burns, incisions and ulcers), while those with
CC immunomodulatory activities may be used in the treatment of viral,
CC bacterial and fungal infections in addition to immune disorders.
CC Polypeptides with growth factor activity may be used in cell cultures to
CC promote cell growth. For example, such polypeptides may be used to
CC manipulate stem cells in culture to give rise to neuroepithelial cells
CC that can be used to augment or replace cells damaged by illness,
CC autoimmune disease or accidental damage. The polypeptides and nucleotides
CC may also be used in the diagnosis of the above conditions, and in drug
CC screening techniques. The present sequence represents a novel human
CC polypeptide of the invention
XX
SQ Sequence 137 AA;

Query Match 39.0%; Score 484; DB 4; Length 137;
Best Local Similarity 96.9%; Pred. No. 2.8e-45;
Matches 94; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```
Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              ||||||||||||||||||||||:||||||||||||||||||||||||||||||||||||||
Db         41 MSIWTSGRTSSSYRHDEKRNIYQRIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 100

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNC 97
              |||||||||||||||||| ||||||||||||||||
Db        101 MXFLLGITLLRSYMQSVWTRESQCTLLNASITETFNC 137
```

RESULT 11
AAB35302
ID AAB35302 standard; protein; 277 AA.
XX
AC AAB35302;
XX
DT 08-MAY-2001 (first entry)
XX
DE Human calcium sensitive potassium channel beta3a subunit.
XX
KW Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW irritable bowel syndrome; Alzheimer's disease.
XX
OS Homo sapiens.
XX
PN WO200105828-A1.
XX
PD 25-JAN-2001.
XX
PF 18-JUL-2000; 2000WO-US019585.
XX
PR 20-JUL-1999; 99US-0144764P.
XX
PA (MERI) MERCK & CO INC.
XX
PI Uebele V, Swanson R, Liu Y, Lagrutta A;
XX
DR WPI; 2001-159514/16.
DR N-PSDB; AAF27992.
XX
PT Novel human calcium sensitive potassium channel subunits for identifying
PT inhibitors and agonists of the potassium channel for use in treating
PT conditions such as asthma, hypertension, memory disorders, depression.
XX
PS Claim 9; Fig 2B; 89pp; English.
XX
CC The present invention provides the protein and coding sequences of the
CC human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC and beta3d subunits. These can be used to identify inhibitors and
CC activators of the channels, which can be used in the treatment of
CC conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC incontinence, migraine and irritable bowel syndrome. The coding sequences
CC are found at human chromosome 3q23-ter. The present sequence is the
CC beta3a subunit
XX
SQ Sequence 277 AA;

Query Match 38.6%; Score 478.5; DB 4; Length 277;
Best Local Similarity 41.3%; Pred. No. 3.3e-44;
Matches 97; Conservative 44; Mismatches 81; Indels 13; Gaps 5;

```
Qy          7 GRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLG 66
              |||:      ::    |    | | ||  | : :   |||||::|| |||  |::|:||||
Db         20 GRTAFPASGKKRETDYS---DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLG 75

Qy         67 ITLLRSYMQSVWTEESQCTLLNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGE 125
              |:|: :| |:  ||| || ::  | : : :|:|:||  |    :||||||:|||:  |:
Db         76 TTILKPFMLSIQREESTCTAIHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQ 135

Qy        126 KLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEG 180
              | ||:: || ::|| || | |||    ::   |:|  ::    : |         |||:  |
Db        136 KALLHYNEEAVQINPKCFYTPKC---HQDRSDLLNSALDIKEFFDHKNGTPFSCFYSPAS 192

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              : ||| | |    :|| ||||:  : ||  || ||:|||:||||||:   : |
Db        193 QSEDVILIKKYDQMAIFHCLFWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 247
```

RESULT 12
AAM78995
ID AAM78995 standard; protein; 277 AA.
XX
AC AAM78995;
XX
DT 06-NOV-2001 (first entry)
XX
DE Human protein SEQ ID NO 1657.
XX
KW Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW tissue growth factor; immunomodulatory; cancer; leukaemia;
KW nervous system disorder; arthritis; inflammation.
XX
OS Homo sapiens.
XX
PN WO200157190-A2.
XX
PD 09-AUG-2001.
XX
PF 05-FEB-2001; 2001WO-US004098.
XX
PR 03-FEB-2000; 2000US-00496914.
PR 27-APR-2000; 2000US-00560875.
PR 20-JUN-2000; 2000US-00598075.
PR 19-JUL-2000; 2000US-00620325.
PR 01-SEP-2000; 2000US-00654936.
PR 15-SEP-2000; 2000US-00663561.
PR 20-OCT-2000; 2000US-00693325.
PR 30-NOV-2000; 2000US-00728422.
XX
PA (HYSE-) HYSEQ INC.
XX
PI Tang YT, Liu C, Drmanac RT, Asundi V, Zhou P, Xu C, Cao Y;
PI Ma Y, Zhao QA, Wang D, Wang J, Zhang J, Ren F, Chen R, Wang ZW;
PI Xue AJ, Yang Y, Wejhrman T, Goodrich R;

```
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK52128.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 4002-4003; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 277 AA;

  Query Match             38.5%;  Score 477.5;  DB 4;  Length 277;
  Best Local Similarity   41.3%;  Pred. No. 4.2e-44;
  Matches   97;  Conservative   44;  Mismatches   81;  Indels   13;  Gaps    5;

Qy          7 GRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLG 66
              |||:      ::   |    | | ||  | : :   |||||::|| |||  |::|:||||
Db         20 GRTAFPASGKKRETDYS---DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLG 75

Qy         67 ITLLRSYMQSVWTEESQCTLLNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGE 125
              |:|: :| |:  ||| || ::  | : : :|:|:||  |    :||||||:|||:  |:
Db         76 TTILKPFMLSIQREESTCTAIHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQ 135

Qy        126 KLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEG 180
              | ||:: || ::|| || | |||    ::   |:|  ::    : |     |||:  |
Db        136 KALLHYNEEAVQINPKCFYTPKC---HQDRNDLLNSALDIKEFFDHKNGTPFSCFYSPAS 192

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
                : ||| | |    :|| |||:  : ||  || ||:|||:||||||:   : |
Db        193 QSEDVILIKKYDQMAIFHCLFWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 247


RESULT 13
ABB11970
ID   ABB11970 standard; peptide; 301 AA.
XX
AC   ABB11970;
XX
DT   11-JAN-2002  (first entry)
XX
DE   Human Ca-activated K channel homologue, SEQ ID NO:2340.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; growth factor;
KW   haematopoiesis regulation; tissue growth; immunomodulator; activin;
KW   inhibin; chemotaxis; chemokinesis; thrombolysis; oncogenesis;
KW   proliferation; metastasis; cancer; tumour; haematopoietic disorder;
KW   myeloid cell disorder; lymphoid cell disorder; asthma; arthritis;
KW   chronic inflammatory condition; proliferative retinopathy;
KW   atherosclerosis; coronary heart disease; arterial ischaemia;
KW   bone disorder; osteoporosis; vascular growth disorder;
KW   tissue regeneration; wound healing; infection; immune disorder;
KW   cell culture; drug screening; gene therapy; antiinflammatory;
KW   antiasthmatic; antiarthritic; haemostatic; antiarteriosclerotic;
KW   cytostatic; osteopathic; vasotropic; cardiant; virucide; antibacterial;
KW   antifungal; vulnerary; antiulcer.
XX
OS   Homo sapiens.
XX
PN   WO200157188-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US003800.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT;
XX
DR   WPI; 2001-457740/49.
DR   N-PSDB; ABA09214.
XX
PT   Human proteins and DNA encoding sequences useful for preventing, treating
PT   or ameliorating a medical condition in a mammalian subject e.g. arthritis
PT   and cancer.
XX
PS   Claim 20; Page 288-289; 1963pp; English.
XX
CC   Sequences ABB10981-ABB12330 represent 1350 novel human polypeptides, and
CC   sequences ABA08225-ABA09574 represent nucleic acids encoding them. The
CC   invention also relates to vectors and recombinant host cells comprising a
CC   nucleotide of the invention, methods of producing the novel polypeptides,
CC   antibodies against the polypeptides, methods of detecting the nucleotides
CC   or polypeptides in a sample, and methods of identifying compounds which
CC   bind to polypeptides of the invention. Although novel, many of the
CC   polypeptides of the invention have homology to known proteins, thereby
CC   giving an insight into their probable biological activities, and hence
CC   potential therapeutic applications. The polypeptides of the invention may
CC   have various activities, including cytokine, cell proliferation or cell
CC   differentiation activities; stem cell growth factor activity;
CC   haematopoiesis regulatory activity; tissue growth activity;
CC   immunomodulatory activity; activin- or inhibin-related activities;
CC   chemotactic or chemokinetic activities; haemostatic, thrombotic or
CC   thrombolytic activities; receptor or ligand activities; or may be
CC   involved in oncogenesis, cancer cell proliferation or metastasis.
CC   Depending on their biological activities, polypeptides and nucleotides of
CC   the invention are useful for preventing, treating or ameliorating medical
CC   conditions, e.g., by protein or gene therapy. Such conditions include
CC   cancers, haematopoietic disorders (e.g.,myeloid or lymphoid cell
CC   disorders), chronic inflammatory conditions (e.g., asthma or arthritis),
CC   proliferative retinopathy, atherosclerosis, coronary heart disease,
CC   arterial ischaemia, bone disorders (e.g., osteoporosis), and abnormal
CC   vascular growth. Polypeptides involved with tissue regeneration and
CC   repair (or nucleic acids encoding them) may be used to promote wound
CC   healing (e.g., of burns, incisions and ulcers), while those with
CC   immunomodulatory activities may be used in the treatment of viral,
CC   bacterial and fungal infections in addition to immune disorders.
CC   Polypeptides with growth factor activity may be used in cell cultures to
CC   promote cell growth. For example, such polypeptides may be used to
CC   manipulate stem cells in culture to give rise to neuroepithelial cells
CC   that can be used to augment or replace cells damaged by illness,
CC   autoimmune disease or accidental damage. The polypeptides and nucleotides
CC   may also be used in the diagnosis of the above conditions, and in drug
CC   screening techniques. The present sequence represents a novel human
CC   polypeptide of the invention
XX
SQ   Sequence 301 AA;

  Query Match             38.5%;  Score 477.5;  DB 4;  Length 301;
  Best Local Similarity   41.3%;  Pred. No. 4.7e-44;
  Matches   97;  Conservative   44;  Mismatches   81;  Indels   13;  Gaps    5;

Qy          7 GRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLG 66
              |||:      ::   |    | | ||  | : :   |||||::|| |||  |::|:||||
Db         44 GRTAFPASGKKRETDYS---DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLG 99

Qy         67 ITLLRSYMQSVWTEESQCTLLNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGE 125
              |:|: :| |:  ||| || ::  | : : :|:|:||  |    :||||||:|||:  |:
Db        100 TTILKPFMLSIQREESTCTAIHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQ 159
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Qy        126 KLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEG 180
              | ||:: || ::|| || | |||    ::   |:|  ::     : |     |||:  |
Db        160 KALLHYNEEAVQINPKCFYTPKC---HQDRNDLLNSALDIKEFFDHKNGTPFSCFYSPAS 216

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
                : ||| | |    :|| ||||:  : ||  || ||:|||:||||||:   : |
Db        217 QSEDVILIKKYDQMAIFHCLFWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 271


RESULT 14
AAM79979
ID   AAM79979 standard; protein; 301 AA.
XX
AC   AAM79979;
XX
DT   06-NOV-2001  (first entry)
XX
DE   Human protein SEQ ID NO 3625.
XX
KW   Human; cytokine; cell proliferation; cell differentiation; gene therapy;
KW   vaccine; peptide therapy; stem cell growth factor; haematopoiesis;
KW   tissue growth factor; immunomodulatory; cancer; leukaemia;
KW   nervous system disorder; arthritis; inflammation.
XX
OS   Homo sapiens.
XX
PN   WO200157190-A2.
XX
PD   09-AUG-2001.
XX
PF   05-FEB-2001; 2001WO-US004098.
XX
PR   03-FEB-2000; 2000US-00496914.
PR   27-APR-2000; 2000US-00560875.
PR   20-JUN-2000; 2000US-00598075.
PR   19-JUL-2000; 2000US-00620325.
PR   01-SEP-2000; 2000US-00654936.
PR   15-SEP-2000; 2000US-00663561.
PR   20-OCT-2000; 2000US-00693325.
PR   30-NOV-2000; 2000US-00728422.
XX
PA   (HYSE-) HYSEQ INC.
XX
PI   Tang YT,  Liu C,  Drmanac RT,  Asundi V,  Zhou P,  Xu C,  Cao Y;
PI   Ma Y,  Zhao QA,  Wang D,  Wang J,  Zhang J,  Ren F,  Chen R,  Wang ZW;
PI   Xue AJ,  Yang Y,  Wejhrman T,  Goodrich R;
XX
DR   WPI; 2001-476283/51.
DR   N-PSDB; AAK53112.
XX
PT   Nucleic acids encoding polypeptides with cytokine-like activities, useful
PT   in diagnosis and gene therapy.
XX
PS   Claim 20; Page 401; 6221pp; English.
XX
CC   The invention relates to polynucleotides (AAK51456-AAK53435) and the
CC   encoded polypeptides (AAM78323-AAM80302) that exhibit activity elating to
CC   cytokine, cell proliferation or cell differentiation or which may induce
CC   production of other cytokines in other cell populations. The
CC   polynucleotides and polypeptides are useful in gene therapy, vaccines or
CC   peptide therapy. The polypeptides have various cytokine-like activities,
CC   e.g. stem cell growth factor activity, haematopoiesis regulating
CC   activity, tissue growth factor activity, immunomodulatory activity and
CC   activin/inhibin activity and may be useful in the diagnosis and/or
CC   treatment of cancer, leukaemia, nervous system disorders, arthritis and
CC   inflammation. Note: Records for SEQ ID NO 2110 (AAK52581), 2111
CC   (AAK52582) and 3666 (AAM80020) are omitted as the relevant pages from the
CC   sequence listing were missing at the time of publication
XX
SQ   Sequence 301 AA;

  Query Match             38.5%;  Score 477.5;  DB 4;  Length 301;
  Best Local Similarity   41.3%;  Pred. No. 4.7e-44;
  Matches   97;  Conservative   44;  Mismatches   81;  Indels   13;  Gaps    5;

Qy          7 GRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLG 66
              |||:      ::   |    | | ||  | : :  |||||::|| |||  |::|:||||
Db         44 GRTAFPASGKKRETDYS---DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLG 99

Qy         67 ITLLRSYMQSVWTEESQCTLLNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGE 125
              |:|: :| |:  ||| || ::  | : : :|:|:|| |    :||||||:|||:  |:
Db        100 TTILKPFMLSIQREESTCTAIHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQ 159

Qy        126 KLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEG 180
              | ||:: || ::|| || | |||    ::   |:|  ::    : |     |||:  |
Db        160 KALLHYNEEAVQINPKCFYTPKC---HQDRNDLLNSALDIKEFFDHKNGTPFSCFYSPAS 216

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
                : ||| | |    :|| ||||:  : ||  || ||:|||:||||||:   : |
Db        217 QSEDVILIKKYDQMAIFHCLFWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 271


RESULT 15
AAB35304
ID   AAB35304 standard; protein; 275 AA.
XX
AC   AAB35304;
XX
DT   08-MAY-2001  (first entry)
XX
DE   Human calcium sensitive potassium channel beta3c subunit.
XX
KW   Human; calcium sensitive potassium channel; beta2 subunit; asthma;
KW   beta3a subunit; beta3b subunit; beta3c subunit; beta3d subunit; diabetes;
KW   chromosome 3q23-ter; inhibitor; activator; glaucoma; migraine; angina;
KW   irritable bowel syndrome; Alzheimer's disease.
XX
OS   Homo sapiens.
XX
PN   WO200105828-A1.
XX
PD   25-JAN-2001.
XX
PF   18-JUL-2000; 2000WO-US019585.
XX
PR   20-JUL-1999;   99US-0144764P.
XX
PA   (MERI ) MERCK & CO INC.
XX
PI   Uebele V,  Swanson R,  Liu Y,  Lagrutta A;
XX
DR   WPI; 2001-159514/16.
DR   N-PSDB; AAF27994.
XX
PT   Novel human calcium sensitive potassium channel subunits for identifying
PT   inhibitors and agonists of the potassium channel for use in treating
PT   conditions such as asthma, hypertension, memory disorders, depression.
XX
PS   Claim 9; Fig 4B; 89pp; English.
XX
CC   The present invention provides the protein and coding sequences of the
CC   human calcium sensitive potassium channel beta2, beta3a, beta3b, beta3c
CC   and beta3d subunits. These can be used to identify inhibitors and
CC   activators of the channels, which can be used in the treatment of
CC   conditions including asthma, diabetes, glaucoma, cerebral ischaemia,
CC   Alzheimer's disease, excessive smooth muscle tone, angina, hypertension,
CC   incontinence, migraine and irritable bowel syndrome. The coding sequences
CC   are found at human chromosome 3q23-ter. The present sequence is the
CC   beta3c subunit
XX
SQ   Sequence 275 AA;

  Query Match             38.3%;  Score 475;  DB 4;  Length 275;
  Best Local Similarity   43.3%;  Pred. No. 7.9e-44;
  Matches   93;  Conservative   41;  Mismatches   71;  Indels   10;  Gaps    4;
```

```
Qy          27 DHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTL 86
               | | ||  | : :   |||||::|| |||  |::|:|||| |:|: :| |:  ||| ||
Db          35 DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLGTTILKPFMLSIQREESTCTA 93

Qy          87 LNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYI 145
               ::  | : : :|:|:||  |    :||||||:|||:  |:| ||:: || ::|| || |
Db          94 IHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQKALLHYNEEAVQINPKCFYT 153

Qy         146 PKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEGNQKSVILTKLYSSNVLFHSL 200
               |||    ::   |:|  ::    : |     |||:  |    : ||| | |    :|| |
Db         154 PKC---HQDRSDLLNSALDIKEFFDHKNGTPFSCFYSPASQSEDVILIKKYDQMAIFHCL 210

Qy         201 FWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
               |||:  : ||  || ||:|||:||||||:   : |
Db         211 FWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 245
```

Search completed: November 6, 2004, 23:31:01
Job time : 71 secs

GenCore version 5.1.6

OM protein - protein search, using sw model

Run on: November 6, 2004, 23:26:11 ; Search time 64 Seconds
(without alignments)
2112.704 Million cell updates/sec

Title: US-09-914-053A-5
Perfect score: 1241
Sequence: 1 MSIWTSGRTSSSYRHDEKRN.....MVKLTQYLSLLCERIQRINR 235

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1825181 seqs, 575374646 residues

Total number of hits satisfying chosen parameters: 1825181

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1235	99.5	235	1	CKB2_HUMAN	Q9y691 h calcium-a
2	1186	95.6	235	1	CKB2_MOUSE	Q9czm9 m calcium-a
3	1185	95.5	235	1	CKB2_RAT	Q811q0 r calcium-a
4	507	40.9	200	1	CKB1_COTJA	Q98855 coturnix co
5	490	39.5	200	2	O93393	O93393 gallus gall
6	474	38.2	279	1	CKB3_HUMAN	Q9npa1 h calcium-a
7	421	33.9	190	1	CKB1_HUMAN	Q16558 h calcium-a
8	421	33.9	191	2	AAS20193	Aas20193 homo sapi
9	418	33.7	190	1	CKB1_RAT	P97678 r calcium-a
10	415	33.4	190	1	CKB1_MOUSE	Q8cae3 m calcium-a
11	406	32.7	190	1	CKB1_RABIT	O46372 o calcium-a
12	396	31.9	190	1	CKB1_CANFA	Q28266 c calcium-a
13	382	30.8	190	1	CKB1_BOVIN	Q28067 b calcium-a
14	316	25.5	210	1	CKB4_HUMAN	Q86w47 h calcium-a
15	312	25.1	210	1	CKB4_RAT	Q9esk8 r calcium-a
16	309	24.9	210	2	Q6QCX8	Q6qcx8 meriones un
17	309	24.9	210	2	AAS55654	Aas55654 meriones
18	308	24.8	210	1	CKB4_MOUSE	Q9jin6 m calcium-a
19	94.5	7.6	482	2	Q8GWP7	Q8gwp7 arabidopsis
20	93.5	7.5	526	2	Q9NJF1	Q9njf1 caenorhabdi
21	92	7.4	897	2	O85661	O85661 proteus mir
22	91.5	7.4	448	2	Q9VZG8	Q9vzg8 drosophila
23	91	7.3	828	2	O94886	O94886 homo sapien
24	90.5	7.3	895	2	Q6FUM7	Q6fum7 candida gla
25	90.5	7.3	895	2	Q9C1S1	Q9c1s1 candida gla
26	89	7.2	286	1	CXA6_RAT	P28233 rattus norv
27	89	7.2	362	1	1B45_HUMAN	P30483 homo sapien
28	89	7.2	550	2	Q6BWP2	Q6bwp2 debaryomyce
29	89	7.2	949	2	Q7RRD8	Q7rrd8 plasmodium
30	88	7.1	362	1	1B44_HUMAN	P30481 homo sapien
31	88	7.1	362	2	Q29849	Q29849 homo sapien
32	88	7.1	563	2	Q8IL46	Q8il46 plasmodium
33	88	7.1	591	2	Q9LL51	Q9ll51 rubus idaeu
34	87.5	7.1	548	2	Q8WWQ1	Q8wwq1 homo sapien
35	87.5	7.1	592	2	Q9HB37	Q9hb37 homo sapien
36	87.5	7.1	592	2	Q8WWQ2	Q8wwq2 homo sapien
37	87.5	7.1	693	2	Q7RKK3	Q7rkk3 plasmodium
38	87.5	7.1	1880	2	O18465	O18465 hirudo medi
39	87	7.0	398	1	HISX_SULSO	O33775 sulfolobus
40	87	7.0	497	2	O01964	O01964 caenorhabdi
41	87	7.0	500	2	Q96CS4	Q96cs4 homo sapien
42	87	7.0	500	2	Q99PJ7	Q99pj7 rattus norv
43	86.5	7.0	438	2	Q91VC4	Q91vc4 mus musculu
44	86	6.9	238	1	CSH2_BOVIN	P19159 bos taurus
45	86	6.9	494	2	O01965	O01965 caenorhabdi

ALIGNMENTS

RESULT 1
CKB2_HUMAN
ID CKB2_HUMAN STANDARD; PRT; 235 AA.
AC Q9Y691;
DT 05-JUL-2004 (Rel. 44, Created)
DT 05-JUL-2004 (Rel. 44, Last sequence update)
DT 01-OCT-2004 (Rel. 45, Last annotation update)
DE Calcium-activated potassium channel beta subunit 2 (Calcium-activated
DE potassium channel, subfamily M, beta subunit 2) (Maxi K channel beta
DE subunit 2) (BK channel beta subunit 2) (Slo-beta 2) (K(VCA)beta 2)
DE (Charybdotoxin receptor beta subunit 2) (BKbeta2) (Hbeta2) (Hbeta3).
GN Name=KCNMB2;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A., FUNCTION, DOMAIN, TISSUE SPECIFICITY, AND
RP INTERACTION WITH KCNMA1.
RC TISSUE=Neuroepithelium;
RX MEDLINE=99199323; PubMed=10097176;
RA Wallner M., Meera P., Toro L.;
RT "Molecular basis of fast inactivation in voltage and Ca2+-activated K+
RT channels: a transmembrane beta-subunit homolog.";
RL Proc. Natl. Acad. Sci. U.S.A. 96:4137-4142(1999).
RN [2]
RP SEQUENCE FROM N.A., AND TISSUE SPECIFICITY.
RC TISSUE=Ovary;
RX MEDLINE=20158960; PubMed=10692449;
RA Brenner R., Jegla T.J., Wickenden A., Liu Y., Aldrich R.W.;
RT "Cloning and functional characterization of novel large conductance
RT calcium-activated potassium channel subunits, hKCNMB3 and hKCNMB4.";
RL J. Biol. Chem. 275:6453-6461(2000).
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Embryonic testis;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;

```
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [4]
RP   FUNCTION, DOMAIN, AND TISSUE SPECIFICITY.
RX   PubMed=10377337;
RA   Xia X.-M., Ding J.-P., Lingle C.J.;
RT   "Molecular basis for the inactivation of Ca2+- and voltage-dependent
RT   BK channels in adrenal chromaffin cells and rat insulinoma tumor
RT   cells.";
RL   J. Neurosci. 19:5255-5264(1999).
RN   [5]
RP   GLYCOSYLATION.
RX   MEDLINE=20266405; PubMed=10792058; DOI=10.1073/pnas.100118597;
RA   Meera P., Wallner M., Toro L.;
RT   "A neuronal beta subunit (KCNMB4) makes the large conductance,
RT   voltage- and Ca2+-activated K+ channel resistant to charybdotoxin and
RT   iberiotoxin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:5562-5567(2000).
RN   [6]
RP   MUTAGENESIS OF 2-PHE--TRP-4.
RX   PubMed=12566540;
RA   Xia X.-M., Ding J.-P., Lingle C.J.;
RT   "Inactivation of BK channels by the NH2 terminus of the beta2
RT   auxiliary subunit: an essential role of a terminal peptide segment of
RT   three hydrophobic residues.";
RL   J. Gen. Physiol. 121:125-148(2003).
RN   [7]
RP   REVIEW.
RX   PubMed=12136044;
RA   Orio P., Rojas P., Ferreira G., Latorre R.;
RT   "New disguises for an old channel: MaxiK channel beta-subunits.";
RL   News Physiol. Sci. 17:156-161(2002).
RN   [8]
RP   STRUCTURE BY NMR OF 1-45.
RX   PubMed=11517232; DOI=10.1074/jbc.M107118200;
RA   Bentrop D., Beyermann M., Wissmann R., Fakler B.;
RT   "NMR structure of the 'ball-and-chain' domain of KCNMB2, the beta 2-
RT   subunit of large conductance Ca2+- and voltage-activated potassium
RT   channels.";
RL   J. Biol. Chem. 276:42116-42121(2001).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Acts as a negative regulator that confers rapid and
CC       complete inactivation of KCNMA1 channel complex. May participate
CC       in KCNMA1 inactivation in chromaffin cells of the adrenal gland or
CC       in hippocampal CA1 neurons.
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB2 per KCNMA1 tetramer.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in kidney, heart and brain. Highly
CC       expressed in ovary. Expressed at low level in other tissues.
CC   -!- DOMAIN: The ball and chain domain mediates the inactivation of
CC       KCNMA1. It occludes the conduction pathway of KCNMA1 channels, and
CC       comprises the pore-blocking ball domain (residues 1-17) and the
CC       chain domain (residues 20-45) linking it to the transmembrane
CC       segment. The ball domain is made up of a flexible N-terminus
CC       anchored at a well ordered loop-helix motif. The chain domain
CC       consists of a 4-turn helix with an unfolded linker at its C-
CC       terminus.
CC   -!- PTM: N-glycosylated.
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF099137; AAD23380.1; -.
DR   EMBL; AF209747; AAF36562.1; -.
DR   EMBL; BC017825; AAH17825.1; -.
DR   PDB; 1JAK; X-ray; A=1-5.
DR   PDB; 1JO6; NMR; A=1-44.
DR   Genew; HGNC:6286; KCNMB2.
DR   MIM; 605214; -.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
DR   GO; GO:0015269; F:calcium-activated potassium channel activity; IDA.
DR   GO; GO:0008200; F:ion channel inhibitor activity; TAS.
DR   GO; GO:0015459; F:potassium channel regulator activity; TAS.
DR   GO; GO:0005513; P:calcium ion sensing; IDA.
DR   GO; GO:0019228; P:generation of action potential; IDA.
DR   GO; GO:0006813; P:potassium ion transport; IDA.
DR   GO; GO:0001508; P:regulation of action potential; IDA.
DR   GO; GO:0019229; P:regulation of vasoconstriction; TAS.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   3D-structure; Glycoprotein; Ionic channel; Transmembrane.
FT   DOMAIN        1     46       Cytoplasmic (Potential).
FT   TRANSMEM     47     67       1 (Potential).
FT   DOMAIN       68    194       Extracellular (Potential).
FT   TRANSMEM    195    215       2 (Potential).
FT   DOMAIN      216    235       Cytoplasmic (Potential).
FT   DOMAIN        1     45       Ball and chain.
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    119    119       N-linked (GlcNAc. . .) (Potential).
FT   MUTAGEN       2      4       FIW->GGG: Abolishes inactivation of
FT                                KCNMA1 channel.
SQ   SEQUENCE   235 AA;  27129 MW;  5752021DF27D8CF5 CRC64;

  Query Match             99.5%;  Score 1235;  DB 1;  Length 235;
  Best Local Similarity   99.6%;  Pred. No. 4.1e-101;
  Matches  234;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120

Qy        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235


RESULT 2
CKB2_MOUSE
ID   CKB2_MOUSE     STANDARD;      PRT;   235 AA.
AC   Q9CZM9;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 2 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 2) (Maxi K channel beta
DE   subunit 2) (BK channel beta subunit 2) (Slo-beta 2) (K(VCA)beta 2)
DE   (Charybdotoxin receptor beta subunit 2) (BKbeta2).
GN   Name=Kcnmb2;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Kidney;
RA   Garcia-Valdes J., Eghbali M., Stefani E., Toro L.;
RT   "Mouse kcnmb2 subunit of the large conductance calcium-activated K
```

```
RT   channel (MaxiK, BK).";
RL   Submitted (NOV-2001) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Embryo;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Brain;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Acts as a negative regulator that confers rapid and
CC       complete inactivation of KCNMA1 channel complex (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB2 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- DOMAIN: The ball and chain domain mediates the inactivation of
CC       KCNMA1. It occludes the conduction pathway of KCNMA1 channels, and
CC       comprises the pore-blocking ball domain (residues 1-17) and the
CC       chain domain (residues 20-45) linking it to the transmembrane
CC       segment. The ball domain is made up of a flexible N-terminus
CC       anchored at a well ordered loop-helix motif. The chain domain
CC       consists of a 4-turn helix with an unfolded linker at its C-
CC       terminus (By similarity).
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY062429; AAL38982.1; -.
DR   EMBL; AK012400; BAB28216.1; -.
DR   EMBL; BC046227; AAH46227.1; -.
DR   EMBL; BC058957; AAH58957.1; -.
DR   HSSP; Q9Y691; 1JO6.
DR   MGD; MGI:1919663; 2700049B16Rik.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   DOMAIN        1     46       Cytoplasmic (Potential).
FT   TRANSMEM     47     67       1 (Potential).
FT   DOMAIN       68    194       Extracellular (Potential).
FT   TRANSMEM    195    215       2 (Potential).
FT   DOMAIN      216    235       Cytoplasmic (Potential).
FT   DOMAIN        1     45       Ball and chain.
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    119    119       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   235 AA;  27119 MW;  F87D3D91C22BBDF2 CRC64;

  Query Match             95.6%;  Score 1186;  DB 1;  Length 235;
  Best Local Similarity   94.9%;  Pred. No. 8.9e-97;
  Matches  223;  Conservative    6;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              | |||||||||||| ||||||||||||||||||||||||||||||||||||||||||||||
Db          1 MFIWTSGRTSSSYRQDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
              |||||||||||||||||||||:|| ||| |||||||||||||||||||||||||||||||
Db         61 MYFLLGITLLRSYMQSVWTEEAQCALLNVSITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120

Qy        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
              |||||:|||||||||:|||||||||||| |||||||||:|||||||::||| |||||||
Db        121 TSSGERLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVSVVMENFRRHQHFPCYSDPEG 180

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235


RESULT 3
CKB2_RAT
ID   CKB2_RAT       STANDARD;      PRT;   235 AA.
AC   Q811Q0; Q8CF83;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 2 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 2) (Maxi K channel beta
DE   subunit 2) (BK channel beta subunit 2) (Slo-beta 2) (K(VCA)beta 2)
DE   (Charybdotoxin receptor beta subunit 2) (BKbeta2) (Rbeta3).
GN   Name=Kcnmb2;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=Sprague-Dawley; TISSUE=Heart;
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RA   Eghbali M., Foroughi S., Toro L., Stefani E.;
RT   "Rat inactivating beta 2 subunit of large conductance Ca2+-activated
RT   K+ channel (KCNMB2, rSlo beta 2 subunit).";
RL   Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE OF 40-201 FROM N.A.
RC   STRAIN=Wistar; TISSUE=Brain;
RX   MEDLINE=22342043; PubMed=12454985; DOI=10.1002/cne.10471;
RA   Langer P., Gruender S., Ruesch A.;
RT   "Expression of a Ca2+-activated BK channel mRNA and its splice
RT   variants in the rat cochlea.";
RL   J. Comp. Neurol. 455:198-209(2003).
RN   [3]
RP   TISSUE SPECIFICITY.
RX   PubMed=10377337;
RA   Xia X.-M., Ding J.-P., Lingle C.J.;
RT   "Molecular basis for the inactivation of Ca2+- and voltage-dependent
RT   BK channels in adrenal chromaffin cells and rat insulinoma tumor
RT   cells.";
RL   J. Neurosci. 19:5255-5264(1999).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Acts as a negative regulator that confers rapid and
CC       complete inactivation of KCNMA1 channel complex (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB2 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- TISSUE SPECIFICITY: Highly expressed in brain and heart. Also
CC       expressed in lung.
CC   -!- DOMAIN: The ball and chain domain mediates the inactivation of
CC       KCNMA1. It occludes the conduction pathway of KCNMA1 channels, and
CC       comprises the pore-blocking ball domain (residues 1-17) and the
CC       chain domain (residues 20-45) linking it to the transmembrane
CC       segment. The ball domain is made up of a flexible N-terminus
CC       anchored at a well ordered loop-helix motif. The chain domain
CC       consists of a 4-turn helix with an unfolded linker at its C-
CC       terminus (By similarity).
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AY191836; AAO43501.1; -.
DR   EMBL; AJ517198; CAD56888.1; -.
DR   HSSP; Q9Y691; 1JO6.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   DOMAIN        1     46       Cytoplasmic (Potential).
FT   TRANSMEM     47     67       1 (Potential).
FT   DOMAIN       68    194       Extracellular (Potential).
FT   TRANSMEM    195    215       2 (Potential).
FT   DOMAIN      216    235       Cytoplasmic (Potential).
FT   DOMAIN        1     45       Ball and chain.
FT   CARBOHYD     88     88       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD     96     96       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    119    119       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     84     84       R -> C (in Ref. 2).
SQ   SEQUENCE   235 AA;  27153 MW;  E111B041867A3F70 CRC64;

  Query Match             95.5%;  Score 1185;  DB 1;  Length 235;
  Best Local Similarity   95.3%;  Pred. No. 1.1e-96;
  Matches  224;  Conservative    5;  Mismatches    6;  Indels    0;  Gaps    0;

Qy          1 MSIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60
              | ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
```

```
Db          1 MFIWTSGRTSSSYRHDEKRNIYQKIRDHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIM 60

Qy         61 MYFLLGITLLRSYMQSVWTEESQCTLLNASITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120
              |||||||||||||||||||:|  ||| ||||||||||||||||||||||||||||||||||
Db         61 MYFLLGITLLRSYMQSVWTEEAQRALLNVSITETFNCSFSCGPDCWKLSQYPCLQVYVNL 120

Qy        121 TSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVVMENFRKYQHFSCYSDPEG 180
              |||||||||||||||:|||||||||||| |||||||||:|||||||::||| |||||||
Db        121 TSSGEKLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVSVVMENFRRHQHFPCYSDPEG 180

Qy        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 NQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235


RESULT 4
CKB1_COTJA
ID   CKB1_COTJA     STANDARD;      PRT;   200 AA.
AC   Q98855;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Putative calcium-activated potassium channel beta subunit.
GN   Name=CO6;
OS   Coturnix coturnix japonica (Japanese quail).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Coturnix.
OX   NCBI_TaxID=93934;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224079; PubMed=9070660;
RA   Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT   "Suppression in transformed avian fibroblasts of a gene (CO6) encoding
RT   a membrane protein related to mammalian potassium channel regulatory
RT   subunits.";
RL   Oncogene 14:1109-1116(1997).
CC   -!- FUNCTION: Probable regulatory subunit of the calcium activated
CC       potassium KCNMA1 (maxiK) channel that modulates the calcium
CC       sensitivity and gating kinetics of KCNMA1, thereby contributing to
CC       KCNMA1 channel diversity. Increases the apparent Ca(2+)/voltage
CC       sensitivity of the KCNMA1 channel (By similarity).
CC   -!- SUBUNIT: Probably interacts with KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U67865; AAC26967.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   DOMAIN        1     19       Cytoplasmic (Potential).
FT   TRANSMEM     20     40       1 (Potential).
FT   DOMAIN       41    166       Extracellular (Potential).
FT   TRANSMEM    167    187       2 (Potential).
FT   DOMAIN      188    200       Cytoplasmic (Potential).
FT   CARBOHYD     89     89       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   200 AA;  22677 MW;  B7A612D8973F711F CRC64;

  Query Match             40.9%;  Score 507;  DB 1;  Length 200;
  Best Local Similarity   47.4%;  Pred. No. 9.2e-37;
  Matches   93;  Conservative   41;  Mismatches   62;  Indels    0;  Gaps    0;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| ||| | || ||: ||| |: ||:|||| :|||:: | :|||| |: | :| |:| :
Db          4 KKLVTAQKRGETRALCLGLGMVACSMMMYFFIGITIVPFYTKSVWTTETICKVLKANIKD 63
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Qy          94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
               :|: | | :   :  ||||||:||||:||::::|||||:|:: | ||||:|   :| :
Db          64 KTHCTNSEGSEDEDIFHYPCLQVWVNLTASGQEVMLYHTEDTLERNPKCSYVPGNSENSK 123

Qy         154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               |  : :  :  ||:||| | || || | | :|||::||    |  :  ||| |  ||  |
Db         124 EVKARIETIASNFKKYQTFPCYYDPGGMQTNVILSRLYPPKGLLFTFLWPTLMFTGGCLI 183

Qy         214 VAMVKLTQYLSLLCER 229
               : :||::|| |:|  |
Db         184 IVLVKISQYFSVLSAR 199


RESULT 5
O93393
ID   O93393      PRELIMINARY;      PRT;   200 AA.
AC   O93393;
DT   01-NOV-1998 (TrEMBLrel. 08, Created)
DT   01-NOV-1998 (TrEMBLrel. 08, Last sequence update)
DT   05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE   Putative calcium-activated potassium channel regulatory subunit
DE   (Calcium-activated potassium channel beta subunit).
GN   Name=CO6;
OS   Gallus gallus (Chicken).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC   Gallus.
OX   NCBI_TaxID=9031;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97224079; PubMed=9070660;
RA   Oberst C., Weiskirchen R., Hartl M., Bister K.;
RT   "Suppression in transformed avian fibroblasts of a gene (CO6) encoding
RT   a membrane protein related to mammalian potassium channel regulatory
RT   subunits.";
RL   Oncogene 14:1109-1116(1997).
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Oberst C., Bister K.;
RL   Submitted (JUL-1998) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RA   Balt S.L., Hudspeth A.J.;
RL   Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AF077369; AAC27490.1; -.
DR   EMBL; AF420468; AAL16898.1; -.
DR   GO; GO:0016020; C:membrane; IEA.
DR   GO; GO:0015269; F:calcium-activated potassium channel activity; IEA.
DR   GO; GO:0005216; F:ion channel activity; IEA.
DR   GO; GO:0006813; P:potassium ion transport; IEA.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
DR   PRINTS; PR01450; BKCHANNELB.
KW   Ionic channel.
SQ   SEQUENCE   200 AA;  22663 MW;  CFD676158C5E0535 CRC64;

  Query Match             39.5%;  Score 490;  DB 2;  Length 200;
  Best Local Similarity   46.4%;  Pred. No. 2.9e-35;
  Matches   91;  Conservative   41;  Mismatches   64;  Indels    0;  Gaps    0;

Qy          34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
               :| ||| | || ||: ||| |: ||:|||| :|||::  | :|||| |: | :|  :| :
Db           4 KKLVTAQKRGETRALCLGLGMVACSMMMYFFIGITIVPFYTKSVWTTETICKVLKVNIKD 63

Qy          94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
               || | | :   :  |||| |:||||:||::::||:|:|:: | ||||:|   :| :
Db          64 KALCSNSEGSEDEDIFHYPCLHVWVNLTASGQEVMLYYTEDTLERNPKCSYVPGNSENAK 123

Qy         154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               |  : :  :  ||:||| | || || | | :|||::||    |  :  ||| |  ||  |
Db         124 EVKAKIEEIANNFKKYQTFPCYYDPGGMQTNVILSRLYPPRGLLFTFLWPTLMFTGGCLI 183

Qy         214 VAMVKLTQYLSLLCER 229
               : :||::||:|:|  |
Db         184 IVLVKISQYVSVLSAR 199


RESULT 6
CKB3_HUMAN
ID   CKB3_HUMAN     STANDARD;      PRT;   279 AA.
AC   Q9NPA1; Q9NPG7; Q9NRM9; Q9UHN3;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 3 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 3) (Maxi K channel beta
DE   subunit 3) (BK channel beta subunit 3) (Slo-beta 3) (K(VCA)beta 3)
DE   (Charybdotoxin receptor beta subunit 3) (BKbeta3) (Hbeta3).
GN   Name=KCNMB3;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 3), AND TISSUE SPECIFICITY.
RX   MEDLINE=20054359; PubMed=10585773; DOI=10.1006/geno.1999.5975;
RA   Riazi M.A., Brinkman-Mills P., Johnson A., Naylor S.L., Minoshima S.,
RA   Shimizu N., Baldini A., McDermid H.E.;
RT   "Identification of a putative regulatory subunit of a calcium-
RT   activated potassium channel in the dup(3q) syndrome region and a
RT   related sequence on 22q11.2.";
RL   Genomics 62:90-94(1999).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 4), TISSUE SPECIFICTY, AND INTERACTION
RP   WITH KCNMA1.
RC   TISSUE=Brain;
RX   MEDLINE=20158960; PubMed=10692449;
RA   Brenner R., Jegla T.J., Wickenden A., Liu Y., Aldrich R.W.;
RT   "Cloning and functional characterization of novel large conductance
RT   calcium-activated potassium channel subunits, hKCNMB3 and hKCNMB4.";
RL   J. Biol. Chem. 275:6453-6461(2000).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4), FUNCTION, ALTERNATIVE
RP   SPLICING, TISSUE SPECIFICITY, AND VARIANT SER-165.
RC   TISSUE=Spleen;
RX   MEDLINE=20390083; PubMed=10766764; DOI=10.1074/jbc.M910187199;
RA   Uebele V.N., Lagrutta A.A., Wade T., Figueroa D.J., Liu Y.,
RA   McKenna E., Austin C.P., Bennett P.B., Swanson R.;
RT   "Cloning and functional expression of two families of Beta-subunits of
RT   the large conductance calcium-activated potassium channel.";
RL   J. Biol. Chem. 275:23211-23218(2000).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND GLYCOSYLATION.
RX   MEDLINE=20266405; PubMed=10792058; DOI=10.1073/pnas.100118597;
RA   Meera P., Wallner M., Toro L.;
RT   "A neuronal beta subunit (KCNMB4) makes the large conductance,
RT   voltage- and Ca2+-activated K+ channel resistant to charybdotoxin and
RT   iberiotoxin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:5562-5567(2000).
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 4).
RX   PubMed=10828459;
RA   Behrens R., Nolting A., Reimann F., Schwarz M., Waldschuetz R.,
RA   Pongs O.;
RT   "hKCNMB3 and hKCNMB4, cloning and characterization of two members of
RT   the large-conductance calcium-activated potassium channel beta subunit
RT   family.";
RL   FEBS Lett. 474:99-106(2000).
RN   [6]
RP   FUNCTION.
RX   PubMed=10864947;
RA   Xia X.-M., Ding J.-P., Zeng X.-H., Duan K.-L., Lingle C.J.;
RT   "Rectification and rapid activation at low Ca2+ of Ca2+-activated,
RT   voltage-dependent BK currents: consequences of rapid inactivation by a
RT   novel beta subunit.";
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RL   J. Neurosci. 20:4890-4903(2000).
RN   [7]
RP   DOMAIN.
RX   PubMed=11382808;
RA   Lingle C.J., Zeng X.-H., Ding J.-P., Xia X.-M.;
RT   "Inactivation of BK channels mediated by the NH(2) terminus of the
RT   beta3b auxiliary subunit involves a two-step mechanism: possible
RT   separation of binding and blockade.";
RL   J. Gen. Physiol. 117:583-606(2001).
RN   [8]
RP   DOMAIN.
RX   PubMed=11382809;
RA   Zeng X.-H., Ding J.-P., Xia X.-M., Lingle C.J.;
RT   "Gating properties conferred on BK channels by the beta3b auxiliary
RT   subunit in the absence of its NH(2)- and COOH termini.";
RL   J. Gen. Physiol. 117:607-628(2001).
RN   [9]
RP   VARIANTS VAL-75; SER-165 AND THR-230.
RX   PubMed=14612589; DOI=10.1152/physiolgenomics.00110.2003;
RA   Hu S., Labuda M.Z., Pandolfo M., Goss G.G., McDermid H.E., Ali D.W.;
RT   "Variants of the KCNMB3 regulatory subunit of maxi BK channels affect
RT   channel inactivation.";
RL   Physiol. Genomics 15:191-198(2003).
RN   [10]
RP   DISULFIDE BONDS, AND DOMAIN.
RX   PubMed=12740608; DOI=10.1038/nsb932;
RA   Zeng X.-H., Xia X.-M., Lingle C.J.;
RT   "Redox-sensitive extracellular gates formed by auxiliary beta subunits
RT   of calcium-activated potassium channels.";
RL   Nat. Struct. Biol. 10:448-454(2003).
RN   [11]
RP   REVIEW.
RX   PubMed=12136044;
RA   Orio P., Rojas P., Ferreira G., Latorre R.;
RT   "New disguises for an old channel: MaxiK channel beta-subunits.";
RL   News Physiol. Sci. 17:156-161(2002).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Alters the functional properties of the current
CC       expressed by the KCNMA1 channel. Isoform 2, isoform 3 and isoform
CC       4 partially inactivate the current of KCNBMA. Isoform 4 induces a
CC       fast and incomplete inactivation of KCNMA1 channel that is
CC       detectable only at large depolarizations. In contrast, isoform 1
CC       does not induce detectable inactivation of KCNMA1. Two or more
CC       subunits of KCNMB3 are required to block the KCNMA1 tetramer.
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB3 per KCNMA1 tetramer.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=4;
CC       Name=1; Synonyms=3d;
CC         IsoId=Q9NPA1-1; Sequence=Displayed;
CC       Name=2; Synonyms=3a;
CC         IsoId=Q9NPA1-2; Sequence=VSP_009827;
CC       Name=3; Synonyms=3c;
CC         IsoId=Q9NPA1-3; Sequence=VSP_009828;
CC       Name=4; Synonyms=3b;
CC         IsoId=Q9NPA1-4; Sequence=VSP_009829, VSP_009830;
CC   -!- TISSUE SPECIFICITY: Isoform 1, isoform 3 and isoform 4 are widely
CC       expressed. Isoform 2 is expressed placenta, pancreas, kidney and
CC       heart. Isoform 1 and isoform 3 are highly expressed in pancreas
CC       and testis.
CC   -!- DOMAIN: The cytoplasmic N-terminus domain of isoform 4
CC       participates to the partial inactivation of KCNMA1, possibly by
CC       binding of to a receptor site.
CC   -!- DOMAIN: The extracellular domain forms gates to block ion
CC       permeation, providing a mechanism by which current can be rapidly
CC       diminished upon cellular repolarization.
CC   -!- PTM: N-glycosylated.
CC   -!- PTM: The extracellular domain contains disulfide bond essential
CC       for the gating mechanism.
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF139471; AAD54771.1; -.
DR   EMBL; AF214561; AAF36598.1; -.
DR   EMBL; AF204159; AAF97031.1; -.
DR   EMBL; AF204160; AAF97032.1; -.
DR   EMBL; AF204161; AAF97033.1; -.
DR   EMBL; AF204162; AAF97034.1; -.
DR   EMBL; AF160968; AAF67811.1; -.
DR   EMBL; AF170916; AAF89698.1; -.
DR   Genew; HGNC:6287; KCNMB3.
DR   MIM; 605222; -.
DR   GO; GO:0016020; C:membrane; NAS.
DR   GO; GO:0015459; F:potassium channel regulator activity; NAS.
DR   GO; GO:0006813; P:potassium ion transport; NAS.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Alternative splicing; Glycoprotein; Ionic channel; Polymorphism;
KW   Transmembrane.
FT   DOMAIN        1     60       Cytoplasmic (Potential).
FT   TRANSMEM     61     81       1 (Potential).
FT   DOMAIN       82    207       Extracellular (Potential).
FT   TRANSMEM    208    228       2 (Potential).
FT   DOMAIN      229    279       Cytoplasmic (Potential).
FT   CARBOHYD    131    131       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC      1     22       MDFSPSSELGFHFVAFILLTRH -> MQPFSIPVQITLQGS
FT                                RRRQG (in isoform 2).
FT                                /FTId=VSP_009827.
FT   VARSPLIC      1     22       MDFSPSSELGFHFVAFILLTRH -> MFPLLYELTAVSPSP
FT                                FPQ (in isoform 3).
FT                                /FTId=VSP_009828.
FT   VARSPLIC      1     22       Missing (in isoform 4).
FT                                /FTId=VSP_009829.
FT   VARSPLIC     23     23       R -> M (in isoform 4).
FT                                /FTId=VSP_009830.
FT   VARIANT      44     44       D -> G (in dbSNP:1170672).
FT                                /FTId=VAR_018173.
FT   VARIANT      53     53       T -> A (in dbSNP:7645550).
FT                                /FTId=VAR_018174.
FT   VARIANT      75     75       L -> V (in dbSNP:2276802).
FT                                /FTId=VAR_018175.
FT   VARIANT     165    165       N -> S.
FT                                /FTId=VAR_018176.
FT   VARIANT     230    230       M -> T.
FT                                /FTId=VAR_018177.
SQ   SEQUENCE   279 AA;  31633 MW;  A6F5A0F64E19AB86 CRC64;

  Query Match             38.2%;  Score 474;  DB 1;  Length 279;
  Best Local Similarity   43.3%;  Pred. No. 1.1e-33;
  Matches   93;  Conservative   41;  Mismatches   71;  Indels   10;  Gaps    4;

Qy         27 DHDLLDKRKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTL 86
              | | ||  | : :   |||||::|| |||  |::|:|||| |:|: :| |:  ||| ||
Db         39 DGDPLDVHKRLPS-STGEDRAVMLGFAMMGFSVLMFFLLGTTILKPFMLSIQREESTCTA 97

Qy         87 LNASITETF-NCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYI 145
              ::  | : : :|:|:||  |    :||||||:|||:  |:| ||:: || ::|| || |
Db         98 IHTDIMDDWLDCAFTCGVHCHGQGKYPCLQVFVNLSHPGQKALLHYNEEAVQINPKCFYT 157

Qy        146 PKCGKNFEESMSLVNVVMENFRKYQH-----FSCYSDPEGNQKSVILTKLYSSNVLFHSL 200
              |||     ::   |:|  ::    : |      |||:  |    : ||| | |    :|| |
Db        158 PKC---HQDRNDLLNSALDIKEFFDHKNGTPFSCFYSPASQSEDVILIKKYDQMAIFHCL 214

Qy        201 FWPTCMMAGGVAIVAMVKLTQYLSLLCERIQRINR 235
              |||:  : ||  || ||:|||:||||||:   : |
Db        215 FWPSLTLLGGALIVGMVRLTQHLSLLCEKYSTVVR 249
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RESULT 7
CKB1_HUMAN
ID   CKB1_HUMAN      STANDARD;      PRT;   190 AA.
AC   Q16558; O00707; O00708; P78475; Q8TAX3; Q93005;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   01-OCT-2004 (Rel. 45, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Hbeta1) (Calcium-
DE   activated potassium channel beta-subunit) (BKbeta) (Slo-beta).
GN   Name=KCNMB1;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Uterus;
RX   MEDLINE=96196569; PubMed=8612769;
RA   Meera P., Wallner M., Jiang Z., Toro L.;
RT   "A calcium switch for the functional coupling between alpha (hslo) and
RT   beta subunits (KV,Ca beta) of maxi K channels.";
RL   FEBS Lett. 382:84-88(1996).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Uterus;
RX   MEDLINE=96335638; PubMed=8764643;
RA   Dworetzky S.I., Boissard C.G., Lum-Ragan J.T., McKay M.C.,
RA   Post-Munson D.J., Trojnacki J.T., Chang C.P., Gribkoff V.K.;
RT   "Phenotypic alteration of a human BK (hSlo) channel by hSlobeta
RT   subunit coexpression: changes in blocker sensitivity,
RT   activation/relaxation and inactivation kinetics, and protein kinase A
RT   modulation.";
RL   J. Neurosci. 16:4543-4550(1996).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Brain;
RX   MEDLINE=96392390; PubMed=8799178;
RA   Tseng-Crank J., Godinot N., Johansen T.E., Ahring P.K., Strobaek D.,
RA   Mertz R., Foster C.D., Olesen S.P., Reinhart P.H.;
RT   "Cloning, expression, and distribution of a Ca(2+)-activated K+
RT   channel beta-subunit from human brain.";
RL   Proc. Natl. Acad. Sci. U.S.A. 93:9200-9205(1996).
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Aortic smooth muscle;
RA   Folander K., Biazzo D., Swanson R.;
RL   Submitted (JUN-1997) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   TISSUE=Myometrium;
RX   PubMed=12434576;
RA   Mazzone J.N., Kaiser R.A., Buxton I.L.;
RT   "Calcium-activated potassium channel expression in human myometrium:
RT   effect of pregnancy.";
RL   Proc. West. Pharmacol. Soc. 45:184-186(2002).
RN   [6]
RP   SEQUENCE FROM N.A. (ISOFORM 2).
RC   TISSUE=Pancreas;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [7]
RP   GLYCOSYLATION.
RX   MEDLINE=20266405; PubMed=10792058; DOI=10.1073/pnas.100118597;
RA   Meera P., Wallner M., Toro L.;
RT   "A neuronal beta subunit (KCNMB4) makes the large conductance,
RT   voltage- and Ca2+-activated K+ channel resistant to charybdotoxin and
RT   iberiotoxin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:5562-5567(2000).
RN   [8]
RP   E2-BINDING.
RX   PubMed=10489376;
RA   Valverde M.A., Rojas P., Amigo J., Cosmelli D., Orio P.,
RA   Bahamonde M.I., Mann G.E., Vergara C., Latorre R.;
RT   "Acute activation of Maxi-K channels (hSlo) by estradiol binding to
RT   the beta subunit.";
RL   Science 285:1929-1931(1999).
RN   [9]
RP   REVIEW.
RX   PubMed=12136044;
RA   Orio P., Rojas P., Ferreira G., Latorre R.;
RT   "New disguises for an old channel: MaxiK channel beta-subunits.";
RL   News Physiol. Sci. 17:156-161(2002).
RN   [10]
RP   VARIANT LYS-64.
RX   PubMed=15057310; DOI=10.1172/JCI200420347;
RA   Fernandez-Fernandez J.M., Tomas M., Vazquez E., Orio P., Latorre R.,
RA   Senti M., Marrugat J., Valverde M.A.;
RT   "Gain-of-function mutation in the KCNMB1 potassium channel subunit is
RT   associated with low prevalence of diastolic hypertension.";
RL   J. Clin. Invest. 113:1032-1039(2004).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate.
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=2;
CC       Name=1;
CC         IsoId=Q16558-1; Sequence=Displayed;
CC       Name=2;
CC         IsoId=Q16558-2; Sequence=VSP_009822, VSP_009823;
CC         Note=No experimental confirmation available;
CC   -!- TISSUE SPECIFICITY: Abundantly expressed in smooth muscle. Low
CC       levels of expression in most other tissues. Within the brain,
CC       relatively high levels found in hippocampus and corpus callosum.
CC   -!- PTM: N-glycosylated.
CC   -!- POLYMORPHISM: Genetic variation in KCNMB1 can influence the
CC       severity of diastolic hypertension.
CC   -!- SIMILARITY: Belongs to the KCNMB family.
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CC   ----------------------------------------------------------------------
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CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; U25138; AAB02394.1; -.
DR   EMBL; U38907; AAA81327.1; -.
DR   EMBL; U42600; AAB16827.1; -.
DR   EMBL; U42601; AAB16825.1; -.
DR   EMBL; U42603; AAB16826.1; -.
DR   EMBL; U42602; AAB16826.1; JOINED.
DR   EMBL; U61536; AAB61396.1; -.
DR   EMBL; U61537; AAB61397.1; -.
DR   EMBL; AF026002; AAB88805.1; -.
DR   EMBL; AY044441; AAK95827.1; -.
DR   EMBL; BC025707; AAH25707.1; -.
DR   PIR; S68842; S68842.
DR   Genew; HGNC:6285; KCNMB1.
DR   MIM; 603951; -.
DR   MIM; 608622; -.
DR   GO; GO:0015269; F:calcium-activated potassium channel activity; TAS.
DR   GO; GO:0015459; F:potassium channel regulator activity; TAS.
DR   GO; GO:0006813; P:potassium ion transport; TAS.
DR   GO; GO:0007268; P:synaptic transmission; TAS.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Alternative splicing; Glycoprotein; Ionic channel; Polymorphism;
KW   Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     17       Cytoplasmic (Potential).
FT   TRANSMEM     18     38       1 (Potential).
FT   DOMAIN       39    156       Extracellular (Potential).
FT   TRANSMEM    157    177       2 (Potential).
FT   DOMAIN      178    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    102    129       CSYIPGSVDNYQTARADVEKVRAKFQEQ -> VLNWRDGDT
FT                                SLYPCQVCEPVPNCPCPRG (in isoform 2).
FT                                /FTId=VSP_009822.
FT   VARSPLIC    130    190       Missing (in isoform 2).
FT                                /FTId=VSP_009823.
FT   VARIANT      64     64       E -> K (has a protective effect against
FT                                diastolic hypertension; dbSNP:11739136).
FT                                /FTId=VAR_019325.
SQ   SEQUENCE   190 AA;  21667 MW;  6DE23A70EF08A2B0 CRC64;

  Query Match             33.9%;  Score 421;  DB 1;  Length 190;
  Best Local Similarity   43.0%;  Pred. No. 3.5e-29;
  Matches   83;  Conservative   40;  Mismatches   62;  Indels    8;  Gaps    2;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | | || ||: ||: |:||::: |::|  |:|  | :||||:||:| |:  :| :
Db          2 KKLVMAQKRGETRALCLGVTMVVCAVITYYILVTTVLPLYQKSVWTQESKCHLIETNIRD 61

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                    |: |||||  :||::::|   :|||||:|   ||:|||||    |::
Db         62 QEELEGK------KVPQYPCL--WVNVSAAGRWAVLYHTEDTRDQNQQCSYIPGSVDNYQ 113

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
                : : |  |   |:: | | |:| | ||: ||:  :||    |  |||||| :: ||: |
Db        114 TARADVEKVRAKFQEQQVFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPTFLLTGGLLI 173

Qy        214 VAMVKLTQYLSLL 226
              :||||  ||||:|
Db        174 IAMVKSNQYLSIL 186


RESULT 8
AAS20193
ID   AAS20193    PRELIMINARY;      PRT;   191 AA.
AC   AAS20193;
DT   02-MAR-2004 (TrEMBLrel. 27, Created)
DT   02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
DT   02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
DE   Large conductance Ca2+-activated K+ channel beta 1 subunit.
GN   KCNMB1.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Pluznick J.L., Sansom S.C.;
RT   "Role of the BK-beta1 subunit in human mesangial cells.";
RL   Submitted (DEC-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY515264; AAS20193.1; -.
KW   Ionic channel.
SQ   SEQUENCE   191 AA;  21797 MW;  547432FF194E770D CRC64;

  Query Match             33.9%;  Score 421;  DB 2;  Length 191;
  Best Local Similarity   43.0%;  Pred. No. 3.5e-29;
  Matches   83;  Conservative   40;  Mismatches   62;  Indels    8;  Gaps    2;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | | || ||: ||: |:||::: |::|  |:|  | :||||:||:| |:  :| :
Db          3 KKLVMAQKRGETRALCLGVTMVVCAVITYYILVTTVLPLYQKSVWTQESKCHLIETNIRD 62

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                    |: |||||  :||::::|   :|||||:|   ||:|||||    |::
Db         63 QEELKGK------KVPQYPCL--WVNVSAAGRWAVLYHTEDTRDQNQQCSYIPGSVDNYQ 114

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
                : : |  |   |:: | | |:| | ||: ||:  :||    |  |||||| :: ||: |
Db        115 TARADVEKVRAKFQEQQVFYCFSAPRGNETSVLFQRLYGPQALLFSLFWPTFLLTGGLLI 174

Qy        214 VAMVKLTQYLSLL 226
              :||||  ||||:|
Db        175 IAMVKSNQYLSIL 187


RESULT 9
CKB1_RAT
ID   CKB1_RAT       STANDARD;      PRT;   190 AA.
AC   P97678; O35337; O88805; Q9ESK7; Q9QWI7;
DT   01-NOV-1997 (Rel. 35, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Calcium-activated
DE   potassium channel beta-subunit) (BKbeta) (Slo-beta) (Slowpoke-beta).
GN   Name=Kcnmb1;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A. (ISOFORM 1), AND TISSUE SPECIFICITY.
RC   STRAIN=Sprague-Dawley;
RX   MEDLINE=97259567; PubMed=9105668;
RA   Chang C.-P., Dworetzky S.I., Wang J., Goldstein M.E.;
RT   "Differential expression of the alpha and beta subunits of the large-
RT   conductance calcium-activated potassium channel: implication for
RT   channel diversity.";
RL   Brain Res. Mol. Brain Res. 45:33-40(1997).
RN   [2]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=Sprague-Dawley; TISSUE=Uterus;
RX   MEDLINE=99107811; PubMed=9888999; DOI=10.1006/geno.1998.5627;
RA   Jiang Z., Wallner M., Meera P., Toro L.;
RT   "Human and rodent MaxiK channel beta-subunit genes: cloning and
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RT   characterization.";
RL   Genomics 55:57-67(1999).
RN   [3]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=Sprague-Dawley; TISSUE=Vascular smooth muscle;
RA   Lange A.R., Gebremedhin D., Aebly M., Harder D.R.;
RL   Submitted (DEC-1996) to the EMBL/GenBank/DDBJ databases.
RN   [4]
RP   SEQUENCE FROM N.A. (ISOFORM 1).
RC   STRAIN=Sprague-Dawley; TISSUE=Uterus;
RA   Reimann F.;
RL   Submitted (NOV-1995) to the EMBL/GenBank/DDBJ databases.
RN   [5]
RP   SEQUENCE FROM N.A. (ISOFORMS 2 AND 3).
RC   TISSUE=Aorta;
RA   Ohya S., Watanabe M., Imaizumi Y.;
RT   "Molecular cloning of a novel spliced variant of calcium activated
RT   potassium channel beta subunit in rat smooth muscle.";
RL   Submitted (FEB-1998) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- ALTERNATIVE PRODUCTS:
CC       Event=Alternative splicing; Named isoforms=3;
CC       Name=1;
CC         IsoId=P97678-1; Sequence=Displayed;
CC       Name=2; Synonyms=1b;
CC         IsoId=P97678-2; Sequence=VSP_009825, VSP_009826;
CC       Name=3; Synonyms=1c;
CC         IsoId=P97678-3; Sequence=VSP_009824, VSP_009825, VSP_009826;
CC   -!- TISSUE SPECIFICITY: Weakly expressed. In brain, it is expressed in
CC       a few discrete populations of neurons that also express KCNMA1.
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
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CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U54498; AAD11548.1; -.
DR   EMBL; AF020712; AAD11858.1; -.
DR   EMBL; U79661; AAB38413.1; -.
DR   EMBL; U40602; AAB96355.1; -.
DR   EMBL; AB010963; BAA33448.1; -.
DR   EMBL; AB050745; BAB17678.1; -.
DR   RGD; 2961; Kcnmb1.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Alternative splicing; Glycoprotein; Ionic channel; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     17       Cytoplasmic (Potential).
FT   TRANSMEM     18     38       1 (Potential).
FT   DOMAIN       39    154       Extracellular (Potential).
FT   TRANSMEM    155    175       2 (Potential).
FT   DOMAIN      176    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
FT   VARSPLIC    102    121       Missing (in isoform 3).
FT                                /FTId=VSP_009824.
FT   VARSPLIC    122    145       VRANFYKHHNFYCFSAPQVNETSV -> LRSRPISSAQQHG
FT                                VTRNGRGPGQA (in isoform 2 and isoform 3).
FT                                /FTId=VSP_009825.
FT   VARSPLIC    146    190       Missing (in isoform 2 and isoform 3).
FT                                /FTId=VSP_009826.
FT   CONFLICT     13     13       T -> A (in Ref. 2).
FT   CONFLICT     27     29       AIT -> VVA (in Ref. 2).
FT   CONFLICT     37     37       V -> M (in Ref. 2).
FT   CONFLICT     55     60       VETNIK -> IESNIR (in Ref. 2).
FT   CONFLICT     68     68       R -> K (in Ref. 2).
FT   CONFLICT     88     88       M -> V (in Ref. 2).
FT   CONFLICT    104    104       Y -> H (in Ref. 1).
FT   CONFLICT    108    110       NLD -> SLE (in Ref. 2).
FT   CONFLICT    114    120       TALVDVK -> VARADVE (in Ref. 2).
FT   CONFLICT    124    124       A -> T (in Ref. 2).
FT   CONFLICT    127    131       YKHHN -> HEHRI (in Ref. 2).
FT   CONFLICT    137    140       APQV -> TTRE (in Ref. 2).
FT   CONFLICT    144    148       SVVYQ -> TVLYR (in Ref. 2).
FT   CONFLICT    155    155       I -> T (in Ref. 2).
FT   CONFLICT    160    160       F -> L (in Ref. 2).
FT   CONFLICT    176    176       M -> I (in Ref. 1).
FT   CONFLICT    179    181       LNR -> INQ (in Ref. 2).
FT   CONFLICT    185    186       VL -> IP (in Ref. 1).
FT   CONFLICT    185    185       V -> I (in Ref. 2).
FT   CONFLICT    190    190       K -> R (in Ref. 1 and 2).
SQ   SEQUENCE   190 AA;  21777 MW;  EA092F4B26FBADDF CRC64;
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Query Match 33.7%; Score 418; DB 1; Length 190;
Best Local Similarity 43.0%; Pred. No. 6.5e-29;
Matches 83; Conservative 42; Mismatches 60; Indels 8; Gaps 2;

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Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
Db          2 KKLVMAQKRGETRALCLGVAMVVCAAITYYILGTTVLPLYQKSVWTQESTCHLVETNIKD 61

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
Db         62 QEEL------EGRKVPQYPCL--WVNVSAVGRWAMLYHTEDTRDQNQQCSYIPRNLDNYQ 113

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
Db        114 TALVDVKKVRANFYKHHNFYCFSAPQVNETSVVYQRLYGPQILLFSFFWPTFLLTGGLLI 173

Qy        214 VAMVKLTQYLSLL 226
Db        174 IAMVKLNRSLSVL 186
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RESULT 10
CKB1_MOUSE
ID   CKB1_MOUSE     STANDARD;      PRT;   190 AA.
AC   Q8CAE3; O35336; O35645;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Calcium-activated
DE   potassium channel beta-subunit) (BKbeta) (Slo-beta).
GN   Name=Kcnmb1;
OS   Mus musculus (Mouse).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX   NCBI_TaxID=10090;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6; TISSUE=Intestinal smooth muscle;
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RX   MEDLINE=99107811; PubMed=9888999; DOI=10.1006/geno.1998.5627;
RA   Jiang Z., Wallner M., Meera P., Toro L.;
RT   "Human and rodent MaxiK channel beta-subunit genes: cloning and
RT   characterization.";
RL   Genomics 55:57-67(1999).
RN   [2]
RP   SEQUENCE FROM N.A.
RC   STRAIN=BALB/c; TISSUE=Heart muscle;
RA   Metzler M.H.F., Repp R., Zibuschka C., Dreyer F., Repp H.;
RT   "Cloning and functional analysis of a calcium activated potassium
RT   channel beta-subunit from murine heart muscle.";
RL   Submitted (AUG-1997) to the EMBL/GenBank/DDBJ databases.
RN   [3]
RP   SEQUENCE FROM N.A.
RC   STRAIN=C57BL/6J; TISSUE=Hypothalamus;
RX   MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
RA   Okazaki Y., Furuno M., Kasukawa T., Adachi J., Bono H., Kondo S.,
RA   Nikaido I., Osato N., Saito R., Suzuki H., Yamanaka I., Kiyosawa H.,
RA   Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schonbach C., Gojobori T.,
RA   Baldarelli R., Hill D.P., Bult C., Hume D.A., Quackenbush J.,
RA   Schriml L.M., Kanapin A., Matsuda H., Batalov S., Beisel K.W.,
RA   Blake J.A., Bradt D., Brusic V., Chothia C., Corbani L.E., Cousins S.,
RA   Dalla E., Dragani T.A., Fletcher C.F., Forrest A., Frazer K.S.,
RA   Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
RA   Grimmond S., Gustincich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
RA   Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
RA   Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
RA   Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
RA   Nagashima T., Numata K., Okido T., Pavan W.J., Pertea G., Pesole G.,
RA   Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
RA   Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
RA   Sandelin A., Schneider C., Semple C.A., Setou M., Shimada K.,
RA   Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
RA   Verardo R., Wagner L., Wahlestedt C., Wang Y., Watanabe Y., Wells C.,
RA   Wilming L.G., Wynshaw-Boris A., Yanagisawa M., Yang I., Yang L.,
RA   Yuan Z., Zavolan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
RA   Hirozane-Kishikawa T., Konno H., Nakamura M., Sakazume N., Sato K.,
RA   Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
RA   Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
RA   Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
RA   Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
RA   Birney E., Hayashizaki Y.;
RT   "Analysis of the mouse transcriptome based on functional annotation of
RT   60,770 full-length cDNAs.";
RL   Nature 420:563-573(2002).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Breast tumor;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   FUNCTION, AND TISSUE SPECIFICITY.
RX   PubMed=11057658; DOI=10.1038/35038011;
RA   Brenner R., Perez G.J., Bonev A.D., Eckman D.M., Kosek J.C.,
RA   Wiler S.W., Patterson A.J., Nelson M.T., Aldrich R.W.;
RT   "Vasoregulation by the beta1 subunit of the calcium-activated
RT   potassium channel.";
RL   Nature 407:870-876(2000).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate.
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Expressed in many tissues containing smooth
CC       muscles. In brain and heart, it is not expressed excpet in the
CC       vasculature, such as cerebral arteries, aorta and corona arteries.
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ----------------------------------------------------------------------
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ----------------------------------------------------------------------
DR   EMBL; AF020711; AAD11857.1; -.
DR   EMBL; AJ001291; CAA04651.1; -.
DR   EMBL; AK038987; BAC30193.1; -.
DR   EMBL; BC013338; AAH13338.1; -.
DR   MGD; MGI:1334203; Kcnmb1.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     17       Cytoplasmic (Potential).
FT   TRANSMEM     18     38       1 (Potential).
FT   DOMAIN       39    154       Extracellular (Potential).
FT   TRANSMEM    155    175       2 (Potential).
FT   DOMAIN      176    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
FT   CONFLICT     92     92       T -> A (in Ref. 1).
FT   CONFLICT    172    172       L -> I (in Ref. 1 and 3).
SQ   SEQUENCE   190 AA;  21714 MW;  924B46FD7EC1910A CRC64;

  Query Match             33.4%;  Score 415;  DB 1;  Length 190;
  Best Local Similarity   43.0%;  Pred. No. 1.2e-28;
  Matches   83;  Conservative   40;  Mismatches   62;  Indels    8;  Gaps    2;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | | || ||: ||:||:||: : |::|| |:|  | :||||:|| | |:  :| :
Db          2 KKLVMAQKRGETRALCLGVAMVVCAAITYYVLGTTVLPLYQKSVWTQESICHLIETNIKD 61

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                          |: ||||| :||::: |   :|||||:|   ||:|||||:   |::
Db         62 QEELEGK------KVPQYPCL--WVNVSAVGRWAMLYHTEDTRDQNQQCSYIPRNLDNYQ 113

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               ::: |  | || |: | | | |: |: ||:  :||   ||  | |||| :: ||: :
Db        114 TALADVKKVRANFYKHHEFYCLSAPQVNETSVVYQRLYGPQVLLFSFFWPTFLLTGGLLL 173

Qy        214 VAMVKLTQYLSLL 226
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              :|||||  :  ||:|
Db        174 IAMVKLNRSLSIL 186


RESULT 11
CKB1_RABIT
ID   CKB1_RABIT     STANDARD;      PRT;   190 AA.
AC   O46372;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Calcium-activated
DE   potassium channel beta-subunit) (BKbeta) (Slo-beta).
GN   Name=KCNMB1;
OS   Oryctolagus cuniculus (Rabbit).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX   NCBI_TaxID=9986;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   STRAIN=New Zealand white; TISSUE=Brain;
RX   PubMed=10821684; DOI=10.1021/bi992865z;
RA   Giangiacomo K.M., Fremont V., Mullmann T.J., Hanner M., Cox R.H.,
RA   Garcia M.L.;
RT   "Interaction of charybdotoxin S10A with single maxi-K channels:
RT   kinetics of blockade depend on the presence of the beta 1 subunit.";
RL   Biochemistry 39:6115-6122(2000).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   PubMed=11294242;
RA   Ohya S., Yamamura H., Muraki K., Watanabe M., Imaizumi Y.;
RT   "Comparative study of the molecular and functional expression of L-
RT   type Ca2+ channels and large-conductance, Ca2+-activated K+ channels
RT   in rabbit aorta and vas deferens smooth muscle.";
RL   Pflugers Arch. 441:611-620(2001).
RN   [3]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Skeletal muscle;
RA   Sakamoto H., Ide T., Kasai M.;
RL   Submitted (NOV-1997) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
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CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF107300; AAD17994.1; -.
DR   EMBL; AB001934; BAA25630.1; -.
DR   EMBL; AB009313; BAA23748.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     14       Cytoplasmic (Potential).
FT   TRANSMEM     15     35       1 (Potential).
FT   DOMAIN       36    156       Extracellular (Potential).
FT   TRANSMEM    157    177       2 (Potential).
FT   DOMAIN      178    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   190 AA;  21697 MW;  687C2F406E5A4FC9 CRC64;

  Query Match             32.7%;  Score 406;  DB 1;  Length 190;
  Best Local Similarity   42.0%;  Pred. No. 7.5e-28;
  Matches   81;  Conservative   42;  Mismatches   62;  Indels    8;  Gaps    2;

Qy          34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
               :| | | | || ||: ||:||::|::: |::|| |:|  | :||||:|| | |:  :| :
Db           2 KKLVMAQKRGETRALCLGVAMVMCAVITYYILGTTMLPLYQKSVWTQESLCRLIETNIRD 61

Qy          94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                          |: |||||  :||::: |:  :|||||||    ||:|||||    |::
Db          62 QEELEGK------KVPQYPCL--WVNVSAVGKWAVLYHTEETRDRNQQCSYIPGSLDNYQ 113

Qy         154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
                ::: |  |    | : | | |:|  : |: ||:  :||     |  ||||||  :: ||: |
Db         114 MALADVEKVRAKFHERQVFYCFSTTQENETSVLYQRLYGPQALLASLFWPTFLLTGGLLI 173

Qy         214 VAMVKLTQYLSLL 226
               :||||: : ||:|
Db         174 IAMVKINRSLSIL 186


RESULT 12
CKB1_CANFA
ID   CKB1_CANFA     STANDARD;      PRT;   190 AA.
AC   Q28266;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Calcium-activated
DE   potassium channel beta-subunit) (BKbeta) (Slo-beta).
GN   Name=KCNMB1;
OS   Canis familiaris (Dog).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX   NCBI_TaxID=9615;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=97053370; PubMed=8897882;
RA   Vogalis F., Vincent T., Qureshi I., Schmalz F.M., Ward M.W.,
RA   Sanders K.M., Horowitz B.;
RT   "Cloning and expression of the large-conductance Ca(2+)-activated K+
RT   channel from colonic smooth muscle.";
RL   Am. J. Physiol. 271:G629-G639(1996).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
```

```
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; U41002; AAA84001.1; -.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Transmembrane.
FT   INIT_MET      0      0       By similarity.
FT   DOMAIN        1     14       Cytoplasmic (Potential).
FT   TRANSMEM     15     35       1 (Potential).
FT   DOMAIN       36    156       Extracellular (Potential).
FT   TRANSMEM    157    177       2 (Potential).
FT   DOMAIN      178    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   190 AA;  21803 MW;  087715070A35D3C8 CRC64;

  Query Match             31.9%;  Score 396;  DB 1;  Length 190;
  Best Local Similarity   40.9%;  Pred. No. 5.8e-27;
  Matches   79;  Conservative   41;  Mismatches   65;  Indels    8;  Gaps    2;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | | || ||: ||:||::|::: |::|| |:|  | :||||::| | |:  :| |
Db          2 KKLVMAQKRGETRALCLGVAMVMCAVIAYYILGTTMLPLYQKSVWTQKSTCHLIETNIRE 61

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                        |: |||||  :||::: |   :|||||:|   | :|||||   :|::
Db         62 QEELEGK------KVPQYPCL--WVNVSAVGRWAVLYHTEDTRDQNHQCSYIPGSLENYQ 113

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               : :  |  |  : |  | |:|    |: :|:  :||   |  ||||| :: ||: |
Db        114 VARADVEKVKAKFHEQQIFYCFSTTRENETTVLYRRLYGPQTLLFSLFWPTFLLTGGLLI 173

Qy        214 VAMVKLTQYLSLL 226
              :||||: | ||:|
Db        174 IAMVKINQSLSIL 186


RESULT 13
CKB1_BOVIN
ID   CKB1_BOVIN     STANDARD;      PRT;   190 AA.
AC   Q28067;
DT   01-NOV-1997 (Rel. 35, Created)
DT   01-NOV-1997 (Rel. 35, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 1 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 1) (Maxi K channel beta
DE   subunit 1) (BK channel beta subunit 1) (Slo-beta 1) (K(VCA)beta 1)
DE   (Charybdotoxin receptor beta subunit 1) (BKbeta1) (Calcium-activated
DE   potassium channel beta-subunit) (BKbeta) (Slo-beta).
GN   Name=KCNMB1;
OS   Bos taurus (Bovine).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC   Bovinae; Bos.
OX   NCBI_TaxID=9913;
RN   [1]
RP   SEQUENCE FROM N.A., AND SEQUENCE OF 1-28.
RC   TISSUE=Aorta, and Trachea;
RX   MEDLINE=94274724; PubMed=8006036;
RA   Knaus H.-G., Folander K., Garcia-Calvo M., Garcia M.L.,
RA   Kaczorowski G.J., Smith M., Swanson R.;
RT   "Primary sequence and immunological characterization of beta-subunit
RT   of high conductance Ca(2+)-activated K+ channel from smooth muscle.";
RL   J. Biol. Chem. 269:17274-17278(1994).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Increases the apparent Ca(2+)/voltage sensitivity of
CC       the KCNMA1 channel. It also modifies KCNMA1 channel kinetics and
CC       alters its pharmacological properties. It slows down the
CC       activation and the deactivation kinetics of the channel. Acts as a
CC       negative regulator of smooth muscle contraction by enhancing the
CC       calcium sensitivity to KCNMA1. Its presence is also a requirement
CC       for internal binding of the KCNMA1 channel opener
CC       dehydrosoyasaponin I (DHS-1) triterpene glycoside and for external
CC       binding of the agonist hormone 17-beta-estradiol (E2). Increases
CC       the binding activity of charybdotoxin (CTX) toxin to KCNMA1
CC       peptide blocker by increasing the CTX association rate and
CC       decreasing the dissociation rate (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB1 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- PTM: N-glycosylated (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; L26101; AAA21741.1; -.
DR   PIR; A54165; A54165.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Direct protein sequencing; Glycoprotein; Ionic channel; Transmembrane.
FT   INIT_MET      0      0
FT   DOMAIN        1     17       Cytoplasmic (Potential).
FT   TRANSMEM     18     38       1 (Potential).
FT   DOMAIN       39    156       Extracellular (Potential).
FT   TRANSMEM    157    177       2 (Potential).
FT   DOMAIN      178    190       Cytoplasmic (Potential).
FT   CARBOHYD     79     79       N-linked (GlcNAc. . .) (Potential).
FT   CARBOHYD    141    141       N-linked (GlcNAc. . .) (Potential).
SQ   SEQUENCE   190 AA;  21826 MW;  288A154B52D06EF8 CRC64;

  Query Match             30.8%;  Score 382;  DB 1;  Length 190;
  Best Local Similarity   40.4%;  Pred. No. 1e-25;
  Matches   78;  Conservative   39;  Mismatches   68;  Indels    8;  Gaps    2;

Qy         34 RKTVTALKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNASITE 93
              :| | | : || ||: ||:||:| ::: |::|| |:|  | :||||:|| | |:  :| :
Db          2 KKLVMAQRRGETRALCLGVAMVVGAVITYYILGTTVLPLYQKSVWTQESTCHLIETNIRD 61

Qy         94 TFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFE 153
                        :: |||||  :||::| |   :|||||:|   | :|||||    |::
Db         62 QEELEGK------RVPQYPCL--WVNVSSVGRWAVLYHTEDTRDQNHQCSYIPSSLDNYQ 113

Qy        154 ESMSLVNVVMENFRKYQHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAI 213
               : :  |  |   | : | | |:|    |: ||:  :||    |  |||||| :: ||: |
Db        114 VARADVEKVRARFHENQDFFCFSTTRENETSVLYRRLYGPQSLLFSLFWPTFLLTGGLLI 173

Qy        214 VAMVKLTQYLSLL 226
              : |||: | ||:|
Db        174 IVMVKINQSLSIL 186


RESULT 14
CKB4_HUMAN
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ID   CKB4_HUMAN     STANDARD;      PRT;   210 AA.
AC   Q86W47; Q8IVR3; Q9NPA4; Q9P0G5;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 4 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 4) (Maxi K channel beta
DE   subunit 4) (BK channel beta subunit 4) (Slo-beta 4) (K(VCA)beta 4)
DE   (Charybdotoxin receptor beta subunit 4) (BKbeta4) (Hbeta4).
GN   Name=KCNMB4;
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A., FUNCTION, GLYCOSYLATION, AND VARIANT ILE-199.
RX   MEDLINE=20266405; PubMed=10792058; DOI=10.1073/pnas.100118597;
RA   Meera P., Wallner M., Toro L.;
RT   "A neuronal beta subunit (KCNMB4) makes the large conductance,
RT   voltage- and Ca2+-activated K+ channel resistant to charybdotoxin and
RT   iberiotoxin.";
RL   Proc. Natl. Acad. Sci. U.S.A. 97:5562-5567(2000).
RN   [2]
RP   SEQUENCE FROM N.A., FUNCTION, AND TISSUE SPECIFICITY.
RX   PubMed=10828459;
RA   Behrens R., Nolting A., Reimann F., Schwarz M., Waldschuetz R.,
RA   Pongs O.;
RT   "hKCNMB3 and hKCNMB4, cloning and characterization of two members of
RT   the large-conductance calcium-activated potassium channel beta subunit
RT   family.";
RL   FEBS Lett. 474:99-106(2000).
RN   [3]
RP   SEQUENCE FROM N.A., FUNCTION, INTERACTION WITH KCNMA1, AND TISSUE
RP   SPECIFICITY.
RX   MEDLINE=20158960; PubMed=10692449;
RA   Brenner R., Jegla T.J., Wickenden A., Liu Y., Aldrich R.W.;
RT   "Cloning and functional characterization of novel large conductance
RT   calcium-activated potassium channel beta subunits, hKCNMB3 and
RT   hKCNMB4.";
RL   J. Biol. Chem. 275:6453-6461(2000).
RN   [4]
RP   SEQUENCE FROM N.A., AND INTERACTION WITH KCNMA1.
RC   TISSUE=CNS;
RX   MEDLINE=20266164; PubMed=10804197;
RA   Weiger T.M., Holmqvist M.H., Levitan I.B., Clark F.T., Sprague S.,
RA   Huang W.-J., Ge P., Wang C., Lawson D., Jurman M.E., Glucksmann M.A.,
RA   Silos-Santiago I., DiStefano P.S., Curtis R.;
RT   "A novel nervous system beta subunit that downregulates human large
RT   conductance calcium-dependent potassium channels.";
RL   J. Neurosci. 20:3563-3570(2000).
RN   [5]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Eye, and Lymph;
RX   MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [6]
RP   PHOSPHORYLATION, AND MUTAGENESIS OF THR-11; SER-17 AND SER-210.
RX   PubMed=11790768; DOI=10.1074/jbc.M107682200;
RA   Jin P., Weiger T.M., Wu Y., Levitan I.B.;
RT   "Phosphorylation-dependent functional coupling of hSlo calcium-
RT   dependent potassium channel and its hbeta 4 subunit.";
RL   J. Biol. Chem. 277:10014-10020(2002).
RN   [7]
RP   GLYCOSYLATION, AND MUTAGENESIS OF ASN-53 AND ASN-90.
RX   PubMed=12223479; DOI=10.1074/jbc.M205795200;
RA   Jin P., Weiger T.M., Levitan I.B.;
RT   "Reciprocal modulation between the alpha and beta 4 subunits of hSlo
RT   calcium-dependent potassium channels.";
RL   J. Biol. Chem. 277:43724-43729(2002).
RN   [8]
RP   REVIEW.
RX   PubMed=12136044;
RA   Orio P., Rojas P., Ferreira G., Latorre R.;
RT   "New disguises for an old channel: MaxiK channel beta-subunits.";
RL   News Physiol. Sci. 17:156-161(2002).
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Decreases the gating kinetics and calcium sensitivity
CC       of the KCNMA1 channel, but with fast deactivation kinetics. May
CC       decrease KCNMA1 channel openings at low calcium concentrations but
CC       increases channel openings at high calcium concentrations. Makes
CC       KCNMA1 channel resistant to 100 nM charybdotoxin (CTX) toxin
CC       concentrations.
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB4 per KCNMA1 tetramer.
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein.
CC   -!- TISSUE SPECIFICITY: Predominantly expressed in brain. In brain, it
CC       is expressed in the cerebellum, cerebral cortex, medulla, spinal
CC       cord, occipital pole, frontal lobe, temporal lobe, putamen,
CC       amygdala, caudate nucleus, corpus callosum, hippocampus,
CC       substantia nigra and thalamus. Weakly or not expressed in other
CC       tissues.
CC   -!- DOMAIN: Resistance to charybdotoxin (CTX) toxin is mediated by the
CC       extracellular domain.
CC   -!- PTM: Phosphorylated. Phosphorylation modulates its effect on
CC       KCNMA1 activation kinetics.
CC   -!- PTM: N-glycosylated. A highly glycosylated form is promoted by
CC       KCNMA1. Glycosylation, which is not required for the interaction
CC       with KCNMA1 and subcellular location, increases protection against
CC       charybdotoxin.
CC   -!- MISCELLANEOUS: Treatment with okadaic acid reduces its effect on
CC       KCNMA1.
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AF160967; AAF69805.1; -.
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DR   EMBL; AF207992; AAF28333.1; -.
DR   EMBL; AF215891; AAF75596.1; -.
DR   EMBL; BC042446; AAH42446.2; -.
DR   EMBL; BC050621; AAH50621.2; -.
DR   Genew; HGNC:6289; KCNMB4.
DR   MIM; 605223; -.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; IDA.
DR   GO; GO:0015269; F:calcium-activated potassium channel activity; IDA.
DR   GO; GO:0005515; F:protein binding; IDA.
DR   GO; GO:0005513; P:calcium ion sensing; IDA.
DR   GO; GO:0019228; P:generation of action potential; IDA.
DR   GO; GO:0006813; P:potassium ion transport; IDA.
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DR   GO; GO:0001508; P:regulation of action potential; IDA.
DR   GO; GO:0046928; P:regulation of neurotransmitter secretion; TAS.
DR   GO; GO:0019229; P:regulation of vasoconstriction; TAS.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Phosphorylation; Polymorphism;
KW   Transmembrane.
FT   DOMAIN        1     19       Cytoplasmic (Potential).
FT   TRANSMEM      20    40       1 (Potential).
FT   DOMAIN        41    167      Extracellular (Potential).
FT   TRANSMEM      168   188      2 (Potential).
FT   DOMAIN        189   210      Cytoplasmic (Potential).
FT   CARBOHYD      53    53       N-linked (GlcNAc. . .).
FT   CARBOHYD      90    90       N-linked (GlcNAc. . .).
FT   VARIANT       199   199      V -> I.
FT                                /FTId=VAR_018178.
FT   MUTAGEN       11    11       T->A: Suppresses the effect of okadaic
FT                                acid and increases activation time
FT                                constant; when associated with A-17 and
FT                                A-210.
FT   MUTAGEN       11    11       T->D: Suppresses its effect on KCNMA1
FT                                channel activation and on deactivation
FT                                kinetics; when associated with E-17 and
FT                                E-210.
FT   MUTAGEN       17    17       S->A: Suppresses the effect of okadaic
FT                                acid and increases activation time
FT                                constant; when associated with A-11 and
FT                                A-210.
FT   MUTAGEN       17    17       S->E: Suppresses its effect on KCNMA1
FT                                channel activation and on deactivation
FT                                kinetics; when associated with D-11 and
FT                                E-210.
FT   MUTAGEN       53    53       N->A: Loss of N-glycosylation and reduced
FT                                protection against charybdotoxin; when
FT                                associated with A-90.
FT   MUTAGEN       90    90       N->A: Loss of N-glycosylation and reduced
FT                                pr$otection against charybdotoxin; when
FT                                associated with A-53.
FT   MUTAGEN       210   210      S->A: Suppresses the effect of okadaic
FT                                acid and increases activation time
FT                                constant; when associated with A-11 and
FT                                A-17.
FT   MUTAGEN       210   210      S->E: Suppresses its effect on KCNMA1
FT                                channel activation and on deactivation
FT                                kinetics; when associated with D-11 and
FT                                E-17.
SQ   SEQUENCE   210 AA;  23948 MW;  A59D56DD034F027A CRC64;

  Query Match           25.5%;  Score 316;  DB 1;  Length 210;
  Best Local Similarity  33.0%;  Pred. No. 7.8e-20;
  Matches   65;  Conservative   40;  Mismatches   80;  Indels   12;  Gaps    3;

Qy         44 EDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNA-SITETFNCSFSCG 102
              ||::| ||| ::: :: |: |  |  :| :  |: ||:|:  | | | |:|:||
Db         14 EDKSIRLGLFLIISGVVSLFIFGFCWLSPALQDLQATEANCTVLSVQQIGEVFECTFTCG 73

Qy        103 PDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGKNFEESMSLVNVV 162
               ||   |||||:||||| : |  : ||:  |  :  | |||||| | :  :::: |
Db         74 ADCRGTSQYPCVQVYVNNSESNSRALLHSDEHQLLTNPKCSYIPPCKRENQKNLESV--- 130

Qy        163 MENFRKY-------QHFSCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVA 215
                |:::|       | |:|| :       |:| : :   || |   ||      || ||
Db        131 -MNWQQYWKDEIGSQPFTCYFNQHQRPDDVLLHRTHDEIVLLHCFLWPLVTFVVGVLIVV 189

Qy        216 MVKLTQYLSLLCERIQR 232
              :   : |::  | :::
Db        190 LTICAKSLAVKAEAMKK 206


RESULT 15
CKB4_RAT
ID   CKB4_RAT       STANDARD;      PRT;   210 AA.
AC   Q9ESK8;
DT   05-JUL-2004 (Rel. 44, Created)
DT   05-JUL-2004 (Rel. 44, Last sequence update)
DT   05-JUL-2004 (Rel. 44, Last annotation update)
DE   Calcium-activated potassium channel beta subunit 4 (Calcium-activated
DE   potassium channel, subfamily M, beta subunit 4) (Maxi K channel beta
DE   subunit 4) (BK channel beta subunit 4) (Slo-beta 4) (K(VCA)beta 4)
DE   (Charybdotoxin receptor beta subunit 4) (BKbeta4).
GN   Name=Kcnmb4;
OS   Rattus norvegicus (Rat).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX   NCBI_TaxID=10116;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Brain;
RA   Ohya S., Ohi Y., Imaizumi Y.;
RT   "rat calcium activated potassium channel beta 4 subunit (KCNMB4).";
RL   Submitted (OCT-2000) to the EMBL/GenBank/DDBJ databases.
RN   [2]
RP   SEQUENCE FROM N.A.
RA   Ha T.S., Park C.-S.;
RT   "Molecular cloning of large-conductance calcium-activated potassium
RT   channel beta 4 subunit from rat brain.";
RL   Submitted (MAR-2001) to the EMBL/GenBank/DDBJ databases.
CC   -!- FUNCTION: Regulatory subunit of the calcium activated potassium
CC       KCNMA1 (maxiK) channel. Modulates the calcium sensitivity and
CC       gating kinetics of KCNMA1, thereby contributing to KCNMA1 channel
CC       diversity. Decreases the gating kinetics and calcium sensitivity
CC       of the KCNMA1 channel, but with fast deactivation kinetics. May
CC       decrease KCNMA1 channel openings at low calcium concentrations but
CC       increases channel openings at high calcium concentrations. Makes
CC       KCNMA1 channel resistant to 100 nM charybdotoxin (CTX) toxin
CC       concentrations (By similarity).
CC   -!- SUBUNIT: Interacts with KCNMA1 tetramer. There are probably 4
CC       molecules of KCMNB4 per KCNMA1 tetramer (By similarity).
CC   -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC   -!- DOMAIN: Resistance to charybdotoxin (CTX) toxin is mediated by the
CC       extracellular domain (By similarity).
CC   -!- PTM: Phosphorylated. Phosphorylation modulates its effect on
CC       KCNMA1 activation kinetics (By similarity).
CC   -!- PTM: N-glycosylated. A highly glycosylated form is promoted by
CC       KCNMA1. Glycosylation, which is not required for the interaction
CC       with KCNMA1 and subcellular location, increases protection against
CC       charybdotoxin (By similarity).
CC   -!- SIMILARITY: Belongs to the KCNMB family.
CC   ---------------------------------------------------------------------
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CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------
DR   EMBL; AB050637; BAB17595.1; -.
DR   EMBL; AY028605; AAK21964.1; -.
DR   RGD; 620728; Kcnmb4.
DR   GO; GO:0008076; C:voltage-gated potassium channel complex; ISS.
DR   GO; GO:0015269; F:calcium-activated potassium channel activity; ISS.
DR   GO; GO:0005515; F:protein binding; ISS.
DR   GO; GO:0005513; P:calcium ion sensing; ISS.
DR   GO; GO:0019228; P:generation of action potential; ISS.
DR   GO; GO:0006813; P:potassium ion transport; ISS.
DR   GO; GO:0001508; P:regulation of action potential; ISS.
DR   GO; GO:0046928; P:regulation of neurotransmitter secretion; ISS.
DR   GO; GO:0019229; P:regulation of vasoconstriction; ISS.
DR   InterPro; IPR003930; BK_channel_beta.
DR   Pfam; PF03185; CaKB; 1.
KW   Glycoprotein; Ionic channel; Phosphorylation; Transmembrane.
FT   DOMAIN        1     19       Cytoplasmic (Potential).
FT   TRANSMEM      20    40       1 (Potential).
FT   DOMAIN        41    167      Extracellular (Potential).
FT   TRANSMEM      168   188      2 (Potential).
```

```
FT   DOMAIN      189    210       Cytoplasmic (Potential).
FT   CARBOHYD     53     53       N-linked (GlcNAc. . .) (By similarity).
FT   CARBOHYD     90     90       N-linked (GlcNAc. . .) (By similarity).
SQ   SEQUENCE   210 AA;  23884 MW;  11D49F58F9C6F1D4 CRC64;

  Query Match             25.1%;  Score 312;  DB 1;  Length 210;
  Best Local Similarity   33.8%;  Pred. No. 1.8e-19;
  Matches   67;  Conservative   39;  Mismatches   78;  Indels   14;  Gaps    4;

Qy         44 EDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEESQCTLLNA-SITETFNCSFSCG 102
              ||::| ||| ::|  |:  |: |   |   :| :    : ||:|:   | | | |:|:||
Db         14 EDKSIRLGLFLIVSGILSLFIFGFCWLSPALQDLQATAANCTVLSVQQIGEVFECTFTCG 73

Qy        103 PDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETIKINQKCSYIPKCGK-NFEESMSLVNV 161
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Job time : 70 secs
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GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 7, 2004, 00:34:47 ; Search time 2961 Seconds
(without alignments)
2892.042 Million cell updates/sec

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Perfect score: 1241
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Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 32822875 seqs, 18219865908 residues

Total number of hits satisfying chosen parameters: 65645750

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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-Q=/cgn2_1/USPTO_spool_p/US09914053/runat_04112004_183922_18233/app_query.fasta_1.391
-DB=EST -QFMT=fastap -SUFFIX=rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

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2: gb_est2:*
3: gb_htc:*
4: gb_est3:*
5: gb_est4:*
6: gb_est5:*
7: gb_est6:*
8: gb_gss1:*
9: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
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2	1186	95.6	2356	3	AK012400	AK012400 Mus muscu
3	1174	94.6	949	5	BQ942589	BQ942589 AGENCOURT
4	1156	93.2	1597	3	AK014106	AK014106 Mus muscu
5	1131.5	91.2	694	7	CK945448	CK945448 4069809 B
6	1123	90.5	803	4	BG198614	BG198614 RST17879
7	1122	90.4	816	4	BG195580	BG195580 RST14773
8	1100.5	88.7	795	4	BG218411	BG218411 RST38279
9	1093.5	88.1	855	5	BU216989	BU216989 603107309
10	1089	87.8	817	4	BG214809	BG214809 RST34463
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13	695	56.0	709	7	CK476300	CK476300 AGENCOURT
14	688	55.4	852	5	BX729097	BX729097 BX729097
15	656	52.9	835	7	CK601161	CK601161 AGENCOURT
16	650	52.4	769	7	CN064012	CN064012 Ag2_p46_A
c 17	648	52.2	622	5	BU950136	BU950136 ic77a08.x
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23	508	40.9	567	2	BF446488	BF446488 7q99h09.x
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30	464	37.4	796	5	BU205207	BU205207 603949389
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ALIGNMENTS

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LOCUS BG188850 801 bp mRNA linear EST 21-APR-2001
DEFINITION RST7884 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION BG188850
VERSION BG188850.1 GI:13710537
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 801)
AUTHORS Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R., Cain,S., Leventhal,C., Thornton,M., Ramachandran,R., Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S., Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K., Offenbacher,J., Danzig,J. and Ducar,M.
TITLE Creation of genome-wide protein expression libraries using random activation of gene expression
JOURNAL Nat. Biotechnol. 19 (5), 440-445 (2001)
MEDLINE 21227151
PUBMED 11329013
COMMENT Contact: Scott J. Cain
Athersys, Inc.
3201 Carnegie Ave, Cleveland, OH 44115, USA
Tel: 216 431 9900
Fax: 216 361 9596
Email: scain@athersys.com
High quality sequence stop: 554.
FEATURES Location/Qualifiers
source 1. .801
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/cell_line="HT1080"
/clone_lib="Athersys RAGE Library"
/note="See 'Creation of Genome-wide Protein Expression Libraries using Random Activation of Gene Expression', Nature Biotechnology, in press. Note that even though the cell type indicated is HT1080, since a random activation method was used, these sequence tags are not necessarily expressed in HT1080 under normal circumstances."

ORIGIN

Alignment Scores:

Pred. No.:	5.08e-131	Length:	801
Score:	1235.00	Matches:	234
Percent Similarity:	99.57%	Conservative:	0
Best Local Similarity:	99.57%	Mismatches:	1
Query Match:	99.52%	Indels:	0
DB:	4	Gaps:	0

US-09-914-053A-5 (1-235) x BG188850 (1-801)

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Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
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Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
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Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
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Db        492 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 551

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 611

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        612 AACCAGAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 671

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        672 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 731

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              ||||||||||||||||||||||||||||||||||||||||||||
Db        732 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 776
```

RESULT 2
AK012400
LOCUS AK012400 2356 bp mRNA linear HTC 03-APR-2004
DEFINITION Mus musculus 11 days embryo whole body cDNA, RIKEN full-length enriched library, clone:2700049B16 product:LARGE CONDUCTANCE CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT, full insert sequence.
ACCESSION AK012400
VERSION AK012400.1 GI:12849119
KEYWORDS HTC; CAP trapper.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1
AUTHORS Carninci,P. and Hayashizaki,Y.
TITLE High-efficiency full-length cDNA cloning
JOURNAL Meth. Enzymol. 303, 19-44 (1999)
MEDLINE 99279253
PUBMED 10349636
REFERENCE 2
AUTHORS Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K., Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
MEDLINE 20499374
PUBMED 11042159
REFERENCE 3
AUTHORS Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P., Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M., Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A., Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K., Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M., Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J., Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
MEDLINE 20530913
PUBMED 11076861
REFERENCE 4
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
TITLE Functional annotation of a full-length mouse cDNA collection
JOURNAL Nature 409, 685-690 (2001)
REFERENCE 5
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs
JOURNAL Nature 420, 563-573 (2002)
REFERENCE 6 (bases 1 to 2356)
AUTHORS Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H., Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y., Furuno,M., Hanagaki,T., Hara,A., Hayatsu,N., Hiramoto,K., Hiraoka,T., Hori,F., Imotani,K., Ishii,Y., Itoh,M., Izawa,M., Kasukawa,T., Kato,H., Kawai,J., Kojima,Y., Konno,H., Kouda,M., Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K., Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C., Saito,H., Saito,R., Sakai,C., Sakai,K., Sano,H., Sasaki,D., Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y., Suzuki,H., Tagami,M., Tagawa,A., Takahashi,F., Tanaka,T., Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K., Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
TITLE Direct Submission
JOURNAL Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp, URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222, Fax:81-45-503-9216)
COMMENT Please visit our web site (http://genome.gsc.riken.jp/) for further details.
cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN.

Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. First strand cDNA was primed with a primer [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was prepared by using trehalose thermo-activated reverse transcriptase and subsequently enriched for full-length by cap-trapper. Second strand cDNA was prepared with the primer adapter of sequence [5' GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI. Host: SOLR.

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FEATURES             Location/Qualifiers
     source          1. .2356
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6J"
                     /db_xref="FANTOM_DB:2700049B16"
                     /db_xref="taxon:10090"
                     /clone="2700049B16"
                     /tissue_type="whole body"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="11 days embryo"
     CDS             242. .949
                     /note="unnamed protein product; LARGE CONDUCTANCE
                     CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT (SPTR|AAL38982,
                     evidence: FASTY, 100%ID, 100%length, match=705)
                     putative"
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                     /protein_id="BAB28216.1"
                     /db_xref="GI:12849120"
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                     PDCWKLSQYPCLQVYVNLTSSGERLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVS
                     VVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVK
                     LTQYLSLLCERIQRINR"
     polyA_signal    2332. .2337
                     /note="putative"
     polyA_site      2356
                     /note="putative"
ORIGIN
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Alignment Scores:
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Score:                  1186.00         Matches:        223
Percent Similarity:     97.45%          Conservative:   6
Best Local Similarity:  94.89%          Mismatches:     6
Query Match:            95.57%          Indels:         0
DB:                     3               Gaps:           0

US-09-914-053A-5 (1-235) x AK012400 (1-2356)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        242 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 301

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        302 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 361

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        362 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 421

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 481

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::||||||   |||||||||   ||||||||||||||||||||||||||||||||||||
Db        482 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 541

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        542 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 601

Qy        121 ThrSerSerGlyGluLysLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||:::||||||||||||||||||||||||||||:::||||||||||||
Db        602 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 661

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||   |||||||||||||||||||||||||||:::
Db        662 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 721

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||:::::|||||||||   ||||||||||||||||||||||
Db        722 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 781

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        782 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 841

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        842 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 901

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db        902 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 946
```

```
RESULT 3
BQ942589
LOCUS       BQ942589                949 bp    mRNA    linear   EST 21-AUG-2002
DEFINITION  AGENCOURT_8888599 NIH_MGC_129 Mus musculus cDNA clone IMAGE:6311623
            5', mRNA sequence.
ACCESSION   BQ942589
VERSION     BQ942589.1  GI:22358067
KEYWORDS    EST.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 949)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Robert Strausberg, Ph.D.
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Susan L. Sullivan, PhD.
             cDNA Library Preparation: ResGen, Invitrogen Corp
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM13735  row: n  column: 08
            High quality sequence start: 36
            High quality sequence stop: 564.
FEATURES             Location/Qualifiers
     source          1. .949
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                     /mol_type="mRNA"
                     /db_xref="taxon:10090"
                     /clone="IMAGE:6311623"
                     /lab_host="DH10B (phage-resistant)"
                     /clone_lib="NIH_MGC_129"
                     /note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;
                     Site_1: EcoRV; Site_2: NotI; Cloned unidirectionally.
                     Primer: Oligo dT. Average insert size 2.2 kb. Constructed
                     by ResGen, Invitrogen Corp. Note: this is a NIH_MGC
                     Library."
ORIGIN
```

```
Alignment Scores:
Pred. No.:              6.72e-124       Length:         949
Score:                  1174.00         Matches:        220
Percent Similarity:     97.84%          Conservative:   6
Best Local Similarity:  95.24%          Mismatches:     5
Query Match:            94.60%          Indels:         0
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DB:                    5              Gaps:          0

US-09-914-053A-5 (1-235) x BQ942589 (1-949)

Qy          4 TrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyrGln 23
              ||||||||||||||||||||||||||||||    |||||||||||||||||||||||||
Db         18 TGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAATATCTACCAG 77

Qy         24 LysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAlaGly 43
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         78 AAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTGAAGGCTGGG 137

Qy         44 GluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPhe 63
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        138 GAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATGATGTACTTC 197

Qy         64 LeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGln 83
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||:::|||
Db        198 CTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAAGAAGCCCAG 257

Qy         84 CysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyPro 103
              |||   |||||||||   ||||||||||||||||||||||||||||||||||||||||||
Db        258 TGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGCTGTGGGCCC 317

Qy        104 AspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSer 123
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        318 GACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTGACATCTTCC 377

Qy        124 GlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSer 143
              ||||||:::||||||||||||||||||||||||||:::|||||||||||||||||||||
Db        378 GGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAAAAGTGCTCC 437

Qy        144 TyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMet 163
              ||||||||||||||||||  ||||||||||||||||||||||||:::|||||||||
Db        438 TATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGTGTCGTCATG 497

Qy        164 GluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLys 183
              ||||||||||||:::::|||||||||   ||||||||||||||||||||||||||||||
Db        498 GAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGAAACCAGAAG 557

Qy        184 SerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpPro 203
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        558 AGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTCTTCTGGCCA 617

Qy        204 ThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeu 223
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        618 ACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACTCAGTACCTC 677

Qy        224 SerLeuLeuCysGluArgIleGlnArgIleAsn 234
              |||||||||||||||||||||||||||||||
Db        678 TCCCTGCTTTGTGAGAGGATCCAACGGATCAAC 710

RESULT 4
AK014106
LOCUS       AK014106               1597 bp    mRNA    linear   HTC 03-APR-2004
DEFINITION  Mus musculus 13 days embryo head cDNA, RIKEN full-length enriched
            library, clone:3110031N04 product:LARGE CONDUCTANCE
            CALCIUM-ACTIVATED K CHANNEL BETA2 SUBUNIT, full insert sequence.
ACCESSION   AK014106
VERSION     AK014106.1  GI:12851769
KEYWORDS    HTC; CAP trapper.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1
  AUTHORS   Carninci,P. and Hayashizaki,Y.
  TITLE     High-efficiency full-length cDNA cloning
  JOURNAL   Meth. Enzymol. 303, 19-44 (1999)
  MEDLINE   99279253
   PUBMED   10349636
REFERENCE   2
  AUTHORS   Carninci,P., Shibata,Y., Hayatsu,N., Sugahara,Y., Shibata,K.,
            Itoh,M., Konno,H., Okazaki,Y., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Normalization and subtraction of cap-trapper-selected cDNAs to
            prepare full-length cDNA libraries for rapid discovery of new genes
  JOURNAL   Genome Res. 10 (10), 1617-1630 (2000)
  MEDLINE   20499374
   PUBMED   11042159
REFERENCE   3
  AUTHORS   Shibata,K., Itoh,M., Aizawa,K., Nagaoka,S., Sasaki,N., Carninci,P.,
            Konno,H., Akiyama,J., Nishi,K., Kitsunai,T., Tashiro,H., Itoh,M.,
            Sumi,N., Ishii,Y., Nakamura,S., Hazama,M., Nishine,T., Harada,A.,
            Yamamoto,R., Matsumoto,H., Sakaguchi,S., Ikegami,T., Kashiwagi,K.,
            Fujiwake,S., Inoue,K., Togawa,Y., Izawa,M., Ohara,E., Watahiki,M.,
            Yoneda,Y., Ishikawa,T., Ozawa,K., Tanaka,T., Matsuura,S., Kawai,J.,
            Okazaki,Y., Muramatsu,M., Inoue,Y., Kira,A. and Hayashizaki,Y.
  TITLE     RIKEN integrated sequence analysis (RISA) system--384-format
            sequencing pipeline with 384 multicapillary sequencer
  JOURNAL   Genome Res. 10 (11), 1757-1771 (2000)
  MEDLINE   20530913
   PUBMED   11076861
REFERENCE   4
  AUTHORS   The RIKEN Genome Exploration Research Group Phase II Team and the
            FANTOM Consortium.
  TITLE     Functional annotation of a full-length mouse cDNA collection
  JOURNAL   Nature 409, 685-690 (2001)
REFERENCE   5
  AUTHORS   The FANTOM Consortium and the RIKEN Genome Exploration Research
            Group Phase I & II Team.
  TITLE     Analysis of the mouse transcriptome based on functional annotation
            of 60,770 full-length cDNAs
  JOURNAL   Nature 420, 563-573 (2002)
REFERENCE   6  (bases 1 to 1597)
  AUTHORS   Adachi,J., Aizawa,K., Akahira,S., Akimura,T., Arai,A., Aono,H.,
            Arakawa,T., Bono,H., Carninci,P., Fukuda,S., Fukunishi,Y.,
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            Koya,S., Kurihara,C., Matsuyama,T., Miyazaki,A., Nishi,K.,
            Nomura,K., Numazaki,R., Ohno,M., Okazaki,Y., Okido,T., Owa,C.,
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            Shibata,K., Shibata,Y., Shinagawa,A., Shiraki,T., Sogabe,Y.,
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            Tejima,Y., Toya,T., Yamamura,T., Yasunishi,A., Yoshida,K.,
            Yoshino,M., Muramatsu,M. and Hayashizaki,Y.
  TITLE     Direct Submission
  JOURNAL   Submitted (10-JUL-2000) Yoshihide Hayashizaki, The Institute of
            Physical and Chemical Research (RIKEN), Laboratory for Genome
            Exploration Research Group, RIKEN Genomic Sciences Center (GSC),
            RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama,
            Kanagawa 230-0045, Japan (E-mail:genome-res@gsc.riken.jp,
            URL:http://genome.gsc.riken.jp/, Tel:81-45-503-9222,
            Fax:81-45-503-9216)
COMMENT     Please visit our web site (http://genome.gsc.riken.jp/) for further
            details.
            cDNA library was prepared and sequenced in Mouse Genome
            Encyclopedia Project of Genome Exploration Research Group in Riken
            Genomic Sciences Center and Genome Science Laboratory in RIKEN.
            Division of Experimental Animal Research in Riken contributed to
            prepare mouse tissues. First strand cDNA was primed with a primer
            [5' GAGAGAGAGAAGGATCCAAGAGCTCTTTTTTTTTTTTTTTVN 3'], cDNA was
            prepared by using trehalose thermo-activated reverse transcriptase
            and subsequently enriched for full-length by cap-trapper. Second
            strand cDNA was prepared with the primer adapter of sequence [5'
            GAGAGAGAGATTCTCGAGTTAATTAAATTAATCCCCCCCCCCCCC 3']. cDNA was cleaved
            with XhoI and SstI. Cloning sites, 5' end: XhoI; 3' end: SstI.
            Host: SOLR.
FEATURES              Location/Qualifiers
     source           1. .1597
                      /organism="Mus musculus"
                      /mol_type="mRNA"
                      /strain="C57BL/6J"
                      /db_xref="FANTOM_DB:3110031N04"
                      /db_xref="taxon:10090"
                      /clone="3110031N04"
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                     /tissue_type="head"
                     /clone_lib="RIKEN full-length enriched mouse cDNA library"
                     /dev_stage="13 days embryo"
     misc_feature    488. .1194
                     /note="LARGE CONDUCTANCE CALCIUM-ACTIVATED K CHANNEL BETA2
                     SUBUNIT (SPTR|AAL38982, evidence: FASTY, 100%ID,
                     100%length, match=705)
                     putative"
ORIGIN

Alignment Scores:
Pred. No.:              1.73e-121      Length:         1597
Score:                  1156.00        Matches:        222
Percent Similarity:     96.60%         Conservative:   5
Best Local Similarity:  94.47%         Mismatches:     8
Query Match:            93.15%         Indels:         1
DB:                     3              Gaps:           0

US-09-914-053A-5 (1-235) x AK014106 (1-1597)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        488 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 547

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        548 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 607

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||   ||||||||||||||||||||||||||||||||||||||
Db        608 AAGGCTGGGGAGGACCGGGACATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 667

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        668 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 727

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||   ||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        728 GAGCC-CAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 786

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        787 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 846

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||:::||||||||||||||||||||||||||:::||||||||||||||
Db        847 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 906

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              |||||||||||||||||||||||||   ||||||||||||||||||||||||||||:::
Db        907 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 966

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              |||||||||||||||||||||||:::::::||||||||   ||||||||||||||||||||
Db        967 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 1026

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1027 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 1086

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       1087 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 1146

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1147 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 1191

RESULT 5
CK945448
LOCUS       CK945448                694 bp    mRNA    linear   EST 15-MAR-2004
DEFINITION  4069809 BARC 10BOV Bos taurus cDNA clone 10BOV17_N10 5', mRNA
            sequence.

ACCESSION   CK945448
VERSION     CK945448.1  GI:45459828
KEYWORDS    EST.
SOURCE      Bos taurus (cow)
  ORGANISM  Bos taurus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
            Bovinae; Bos.
REFERENCE   1  (bases 1 to 694)
  AUTHORS   Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay,
            G.P., Bosak, S., Rubenfield, M. and Gasbarre, L.C.
  TITLE     Production of EST from cDNA libraries derived from immunologically
            activated bovine gut
  JOURNAL   Unpublished (2004)
COMMENT     Contact: Tad S. Sonstegard
            Bovine Functional Genomics Laboratory
            Animal and Natural Resources Institute
            Bdlg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA
            Tel: 3015048416
            Fax: 3015048414
            Email: tads@anri.barc.usda.gov
            Single pass sequencing. Bases called and trimmed with phred
            0.000925 using options -trim_alt " -trim_fasta. Vector identified
            by cross_match using options -minmatch 12 -minscore 12
            Plate: 17  row: N  column: 10
            Seq primer: CCCAGTCACGACGTTGTAAAACG
            High quality sequence stop: 694.
FEATURES             Location/Qualifiers
     source          1. .694
                     /organism="Bos taurus"
                     /mol_type="mRNA"
                     /strain="Holstein"
                     /db_xref="taxon:9913"
                     /clone="10BOV17_N10"
                     /sex="Male"
                     /tissue_type="Pooled"
                     /dev_stage="Multiple"
                     /lab_host="DH10B T1 phage resistant"
                     /clone_lib="BARC 10BOV"
                     /note="Organ: Small Intestine; Vector: pAgen-1; Site_1:
                     EcoRV; Site_2: NotI; Equimolar amounts of mRNA extracted
                     from proximal jejunums of 18 and 21 wk old steers, and
                     distal ileums of 14 day old calves. proximal jejunum
                     exposed to C. oncophora for 3 and 6 weeks, and distal
                     ileum exposed to C. parvum for 7 days"
ORIGIN

Alignment Scores:
Pred. No.:              3.21e-119      Length:         694
Score:                  1131.50        Matches:        220
Percent Similarity:     98.66%         Conservative:   1
Best Local Similarity:  98.21%         Mismatches:     3
Query Match:            91.18%         Indels:         2
DB:                     7              Gaps:           0

US-09-914-053A-5 (1-235) x CK945448 (1-694)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         17 ATGTTTATATGGACCAGTGGCCGGACTTCTTCATCTTACAGACATGATGAGAAAAGAAAT 76

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         77 ATTTACCAAAAAATCAGGGACCACGACCTCCTGGACAAAAGGAAAACTGTCACAGCACTG 136

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        137 AAAGCAGGAGAGGACCGGGCCATTCTCCTGGGACTGGCCATGATGGTGTGCTCCATCATG 196

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        197 ATGTACTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGTGTATGGACCGAG 256
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Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::|||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        257 GAGGCTCAGTGCACCTTGCTGAATGCATCCATCACAGAAACATTTAACTGCTCCTTCAGC 316

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        317 TGTGGTCCGGACTGCTGGAAACTCTCTCAGTATCCCTGCCTACAGGTGTATGTTAACCTG 376

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        377 ACTTCTTCCGGTGAAAAGCTCCTTCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 436

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        437 AAGTGCTCCTATATACCTAAGTGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 496

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        497 GTTGTCATGGAAAACTTCAGGAAGTACCAACACTTCTCCTGCTACTCTGACCCGGAAGGA 556

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        557 AACCAGAAGAGTGTCATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 616

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              |||||||||||||||||||||||||||||||||||||   |||||||||   ||||||
Db        617 TTTTGGCCAACATGCATGATGGCTGGGGGCGTGGCAATTGT-GCCATGGTGAA-CTCACA 674

Qy        221 GlnTyrLeuSer 224
              ||||||||||||
Db        675 CAGTATCTTTCC 686

RESULT 6
BG198614
LOCUS       BG198614                803 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST17879 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG198614
VERSION     BG198614.1  GI:13720301
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 803)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 553.
FEATURES             Location/Qualifiers
     source          1. .803
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

Alignment Scores:
Pred. No.:                3.8e-118      Length:          803
Score:                    1123.00       Matches:         217
Percent Similarity:       94.02%        Conservative:    3
Best Local Similarity:    92.74%        Mismatches:      13
Query Match:              90.49%        Indels:          1
DB:                       4             Gaps:            0

US-09-914-053A-5 (1-235) x BG198614 (1-803)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         73 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 132

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        133 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 192

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||:::||||||||||||||||||||||||||||||||||||||||||||||
Db        193 AAGGCAGGAGAGGAACGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 252

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        253 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 312

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        313 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATCTAATTGCTCCTTCAGC 372

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        373 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 432

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        433 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 492

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        493 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGCCCCTGGTGAAT 552

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        553 GTTGTCATGGAAAACTTCAGGAAGCATCAACACTTCTCCTGCTATTCTGACCCAGAACGA 612

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        613 AACCAGAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGGGCTGTTCCATTCACTC 672

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetVal-LysLeuTh 220
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        673 TTCTGGCCAACCTGTATGATGGCTGGGGGTGGGGGAATTGGTTGCATGGTGGGAACTTCA 732

Qy        220 rGlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIle 233
              |||   ||||||||||||||||||||||   ||||||
Db        733 CCAGTCCTTTTCCCTACTATGTGAGAGGATCCACCGGATC 772

RESULT 7
BG195580
LOCUS       BG195580                816 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST14773 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG195580
VERSION     BG195580.1  GI:13717267
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 816)
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```
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 364.
FEATURES             Location/Qualifiers
     source          1. .816
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

Alignment Scores:
Pred. No.:                5.07e-118      Length:          816
Score:                    1122.00        Matches:         220
Percent Similarity:       93.25%         Conservative:    1
Best Local Similarity:    92.83%         Mismatches:      14
Query Match:              90.41%         Indels:          2
DB:                       4              Gaps:            0

US-09-914-053A-5 (1-235) x BG195580 (1-816)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||:::|||||||||||||||||||||||||||||||||||||
Db         72 ATGTTTATATGGACCAGTGGCCAGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 131

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 251

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 311

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGC 371

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 431

Qy        121 ThrSerSerGlyGluLysLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ACTTCTTNCGGNGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 491

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        492 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTNCCTGGTGAAT 551

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        552 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 611

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsn-ValLeuPheHisSerLe 200
              ||||||||||||||||  ||||||||||||||||||||||| |||       ||||||||
Db        612 AACCAGAAGAGTGTTATNCTAACAAAACTCTACAGTTCCAACCGTGCNTGTCCATTCACT 671

Qy        200 uPheTrpProThrCysMetMet-AlaGlyGlyValAlaIleValAlaMetValLysLeuT 220
              |   |||   |||||||||||| ||||||||||||   ||||||||||||||||||||||
Db        672 TCTCTGGCAAACCTGTATGATGGGCTGGGGGCGTGCAAATTGTTGCCATGGTGAAACTTA 731

Qy        220 hrGlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||   |||   |||||||   ||||||||||||   |||   |||
Db        732 CACAGGACCTCTNCCTACTATGGGAGAGGATCCAACCGATCANTAGA 778

RESULT 8
BG218411
LOCUS       BG218411                 795 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST38279 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG218411
VERSION     BG218411.1  GI:13744560
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 795)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 483.
FEATURES             Location/Qualifiers
     source          1. .795
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

Alignment Scores:
Pred. No.:                1.44e-115      Length:          795
Score:                    1100.50        Matches:         222
Percent Similarity:       95.71%         Conservative:    1
Best Local Similarity:    95.28%         Mismatches:      8
Query Match:              88.68%         Indels:          4
DB:                       4              Gaps:            1

US-09-914-053A-5 (1-235) x BG218411 (1-795)

Qy          3 IleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsnIleTyr 22
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Db        78 ATATGGACCAGCGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAATATTTAC 137

Qy        23 GlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeuLysAla 42
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       138 CAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTGAAGGCA 197

Qy        43 GlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyr 62
             ||||||||||||||||  ||||||||||||||||||||||||||||||||||||||||||
Db       198 GGAGAGGACCGAGCTTTTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTAT 257

Qy        63 PheLeuLeuGlyIleThrLeu-LeuArgSerTyrMetGlnSerValTrpThrGluGluSe 82
             ||||||||||||      ||| ||||||||||||||||||||||||||||||||||||||
Db       258 TTTCTGCTGGGATTT---CTTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTC 314

Qy        82 rGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGl 102
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       315 TCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGG 374

Qy       102 yProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSe 122
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       375 TCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTC 434

Qy       122 rSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCy 142
             |||||||  ||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       435 TTCCGGGGA-AAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTG 493

Qy       142 sSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValVa 162
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       494 CTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGT 553

Qy       162 lMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGl 182
             ||||||||||||  ||||||||||||||||  ||||||||||||||||||||||||||||
Db       554 CATGGAAAACTTCACGAAGTATCAACACTTCTTCTGCTATTCTGACCCAGAAGGAAACCA 613

Qy       182 nLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTr 202
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       614 GAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTTTTCTG 673

Qy       202 pProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTy 222
             |||||||  ||||||||||||||||||||||||||||||  |||  |||||||||||||
Db       674 GCCAACCTGGATGATGGCTGGCGGGGTGGCAATTGTTGCCATGGGGAAACT-ACACAGTA 732

Qy       222 rLeuSerLeuLeuCysGluArgIleGlnArgIleAsn 234
             |||||||||||||||||||||||||||||||:::
Db       733 CCTTTCCCTACTATGTGAGAGGATCCAACGGATCCAT 769
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RESULT 9
BU216989

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LOCUS       BU216989                855 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  603107309F1 CSEQCHN04 Gallus gallus cDNA clone ChEST48b4 5', mRNA
            sequence.
ACCESSION   BU216989
VERSION     BU216989.1  GI:25398033
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 855)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .855
                     /organism="Gallus gallus"
                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="ChEST48b4"
                     /tissue_type="whole embryo"
                     /dev_stage="20-21"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN04"
                     /note="Organ: whole embryo; Vector: pBluescript II KS(+);
                     Site_1: EcoRI; Site_2: Not1; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN
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Alignment Scores:

Pred. No.:	1.03e-114	Length:	855
Score:	1093.50	Matches:	209
Percent Similarity:	93.64%	Conservative:	12
Best Local Similarity:	88.56%	Mismatches:	7
Query Match:	88.11%	Indels:	8
DB:	5	Gaps:	1

US-09-914-053A-5 (1-235) x BU216989 (1-855)

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Qy         1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
             |||   |||||||||||||||||:::|||:::|||||||||||||||||||||
Db       152 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 205

Qy        21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
                                 ||||||||||||||||||||||||||||||||||||||||
Db       206 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 250

Qy        41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       251 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 310

Qy        61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
             ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db       311 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 370

Qy        81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
             |||:::||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db       371 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 430

Qy       101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
             ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db       431 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 490

Qy       121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
             ||||||||||||:::|||||||||||||||||||||||||||||||:::|||||||||
Db       491 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 550

Qy       141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
             :::|||||||||||||||||||||||||||||||:::|||||||||||||||:::||||||
Db       551 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 610

Qy       161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
             ||||||||||||||||||||||||||||||  ||||||||||:::  ||||||||||||
Db       611 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 670
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```
Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||:::||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        671 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 730

Qy        201 PheTrpProThrCysMetMetAlaGlyGly-ValAlaIleValAlaMetValLysLeuTh 220
              ||||||||||||||||||||    |||||| ||||||||||||||||||||||||||||||
Db        731 TTCTGGCCCACGTGCATGATGATCGGCGGCCGTTGCCATTGTTGCGATGGTAAAGCTGAC 790

Qy        220 rGlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              ||||||||||||||||||    ||||||||||||||||||||||
Db        791 TCAATACCTTTCTCTCCTCTGGGAGAGAATCCAAAGGATCAACAGA 836

RESULT 10
BG214809
LOCUS       BG214809                817 bp    mRNA    linear   EST 21-APR-2001
DEFINITION  RST34463 Athersys RAGE Library Homo sapiens cDNA, mRNA sequence.
ACCESSION   BG214809
VERSION     BG214809.1  GI:13740830
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 817)
  AUTHORS   Harrington,J.J., Sherf,B., Rundlett,S., Jackson,P.D., Perry,R.,
            Cain,S., Leventhal,C., Thornton,M., Ramachandran,R.,
            Whittington,J., Lerner,L., Costanzo,D., McElligott,K., Boozer,S.,
            Mays,R., Smith,E., Veloso,N., Klika,A., Hess,J., Cothren,K., Lo,K.,
            Offenbacher,J., Danzig,J. and Ducar,M.
  TITLE     Creation of genome-wide protein expression libraries using random
            activation of gene expression
  JOURNAL   Nat. Biotechnol. 19 (5), 440-445 (2001)
  MEDLINE   21227151
   PUBMED   11329013
COMMENT     Contact: Scott J. Cain
            Athersys, Inc.
            3201 Carnegie Ave, Cleveland, OH 44115, USA
            Tel: 216 431 9900
            Fax: 216 361 9596
            Email: scain@athersys.com
            High quality sequence stop: 364.
FEATURES             Location/Qualifiers
     source          1. .817
                     /organism="Homo sapiens"
                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /cell_line="HT1080"
                     /clone_lib="Athersys RAGE Library"
                     /note="See 'Creation of Genome-wide Protein Expression
                     Libraries using Random Activation of Gene Expression',
                     Nature Biotechnology, in press. Note that even though the
                     cell type indicated is HT1080, since a random activation
                     method was used, these sequence tags are not necessarily
                     expressed in HT1080 under normal circumstances."
ORIGIN

Alignment Scores:
Pred. No.:              3.15e-114       Length:         817
Score:                  1089.00         Matches:        220
Percent Similarity:     94.56%          Conservative:   6
Best Local Similarity:  92.05%          Mismatches:     9
Query Match:            87.75%          Indels:         5
DB:                     4               Gaps:           0

US-09-914-053A-5 (1-235) x BG214809 (1-817)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db         72 ATGTTTATATGGACCAGTGGCCAGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 131

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        132 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 191

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        192 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 251

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        252 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 311

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        312 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGC 371

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        372 TGTGGTCCAGACTGCTGGAAACTNTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 431

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        432 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 491

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSer-LeuValAs 160
              ||||||||||||||||||    ||||||||||||  |||:::|||||||| ||||||||
Db        492 AAGTGCTCCTATATACCTANATGTGGAAAAAATTNTGAAGATTCCATGTCCCCTGGTGAA 551

Qy        160 nValVal-MetGluAsnPheArgLysTyrGlnHis-PheSerCysTyrSerAspProGlu 179
              ||||||| :::|||||||||||||||||   |||||| ||||||||||||||||||||||
Db        552 TGTTGTCATTGGAAAACTTCAGGAAGGATCAACACTTTTTCCTGTTATTCTGACCCAGAA 611

Qy        180 GlyAsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSer 199
              ||||||||||||||   ||||||||||||||||||||||||||||   ||||||||
Db        612 GGAAACCAGAAGAGTGGTATCCTAACCAAACTCTACAGTTCCAACGG-CTGTTCCATTTA 670

Qy        200 LeuPheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetVal-LysLe 219
              ||||||||||||||||||:::|||||||||||  ||||||||||:::||| ||||||
Db        671 CTCTTTTGGCCAACCTGTTTGATGGCTGGGGGGCGTGCAATTGTTGCCCTTGTGAAAACT 730

Qy        219 uThrGlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              ||||||||||||||||||||||||||||||||||||||||||||||||:::
Db        731 AACACAGTACCTTTCCCTACTATGTGAGAGGATCCACCGGATCAATAAA 779

RESULT 11
BU222329
LOCUS       BU222329                939 bp    mRNA    linear   EST 25-NOV-2002
DEFINITION  603105389F1 CSEQCHN04 Gallus gallus cDNA clone ChEST43b24 5', mRNA
            sequence.
ACCESSION   BU222329
VERSION     BU222329.1  GI:25411618
KEYWORDS    EST.
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 939)
  AUTHORS   Boardman,P.E., Sanz-Ezquerro,J., Overton,I.M., Burt,D.W., Bosch,E.,
            Fong,W.T., Tickle,C., Brown,W.R.A., Wilson,S.A. and Hubbard,S.J.
  TITLE     A Comprehensive Collection of Chicken cDNAs
  JOURNAL   Curr. Biol. 12 (22), 1965-1969 (2002)
  MEDLINE   22335534
   PUBMED   12445392
COMMENT     Contact: Simon Hubbard
            Department of Biomolecular Sciences
            University of Manchester Institute of Science and Technology
            (UMIST)
            PO Box 88, Manchester, M60 1QD, UK
            Tel: 01612008930
            Fax: 01612360409
            Email: Simon.Hubbard@umist.ac.uk.
FEATURES             Location/Qualifiers
     source          1. .939
                     /organism="Gallus gallus"
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                     /strain="White Leghorn, Hisex"
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                     /tissue_type="whole embryo"
                     /dev_stage="20-21"
                     /lab_host="DH10B"
                     /clone_lib="CSEQCHN04"
                     /note="Organ: whole embryo; Vector: pBluescript II KS(+);
                     Site_1: EcoRI; Site_2: NotI; This normalized library was
                     constructed from 1 million independent clones. cDNA
                     synthesis was initiated using an oligo(dT) primer, using
                     methylated C in the first strand synthesis reaction.
                     Following this first strand reaction, double-stranded cDNA
                     was blunted, ligated to NotI adapters, digested with
                     EcoRI, size-selected, and cloned into the NotI and EcoRI
                     compatible sites of a custom modified MCS of the
                     pBluescript (KS+) vector. The library was normalized in 2
                     rounds using conditions adapted from Soares et al., PNAS
                     (1994) 91: 9228-9232 and Bonaldo et al., Genome Research 6
                     (1996): 791, except that a significantly longer
                     reannealing hybridization was used."
ORIGIN

Alignment Scores:
Pred. No.:              9.52e-101      Length:          939
Score:                  972.50         Matches:         205
Percent Similarity:     88.98%         Conservative:    13
Best Local Similarity:  83.67%         Mismatches:      10
Query Match:            78.36%         Indels:          17
DB:                     5              Gaps:            3

US-09-914-053A-5 (1-235) x BU222329 (1-939)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||:::|||:::|||||||||||||||||||||
Db        152 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 205

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
                                 ||||||||||||||||||||||||||||||||||||||||
Db        206 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 250

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        251 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 310

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        311 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 370

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::||||||:::||||||||||||||||||||||||||||||||||||||||||||
Db        371 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 430

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||:::||||||||||||||||||||||||||||||||||||
Db        431 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 490

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLys-IleAsnGl 140
              ||||||||||:::|||||||||||||||||||||||||||||:::|||| ||||||
Db        491 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAACATTAATTC 550

Qy        140 nLysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAs 160
              :::|||||||||||||||||||||||||||||:::|||||||||||||||:::|||||
Db        551 TGAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAA 610

Qy        160 nValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGl 180
              |||||||||||||||||||||||||||||   |||||||||:::   ||||||||||
Db        611 CGTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGG 670

Qy        180 yAsnGlnLysSerValIleLeuThr-LysLeuTyrSerSer-AsnVal---LeuPheHis 198
              |   ||||||:::|||||||||||| |||||||||||||| ||||||         |||
Db        671 CACTCAGAAGAACGTGATATTGACCAAAACTGTACAGCTCCCAACGTGGCTTGTTCACAC 730

Qy        199 SerLeuPheTrp--ProThrCysMetMetAlaGlyGlyValAla---IleValAlaMetV 217
              ||||||||||||  ||||||||||||||||    ||||||||||||      :::   ||||
Db        731 TCGCTCTTCTGGGCCCCACGTGCATGATGATCGGCGGCGTTGCCCATTGTTTGCGAATGG 790

Qy        217 alLys-LeuThrGlnTyrLeu-SerLeuLeuCysGluArgIle-GlnArgIleAsnArg 235
              ||||| |||||||||||||||| |||||||||||||||||||| ||||||||||||||
Db        791 TAAAGCCTGACTCAATACCTTTTCTCTCCTCTGCGAGAGAATCCCAAAGGATCAACAGA 849

RESULT 12
CK903430/c
LOCUS       CK903430                598 bp    mRNA    linear   EST 11-MAR-2004
DEFINITION  ie57a02.x5 Melton Normalized Human Islet 4 N4-HIS 1 Homo sapiens
            cDNA clone IMAGE:5670818 3' similar to TR:Q9Y691 Q9Y691 MAXIK
            CHANNEL BETA 2 SUBUNIT. ;, mRNA sequence.
ACCESSION   CK903430
VERSION     CK903430.1  GI:45364961
KEYWORDS    EST.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 598)
  AUTHORS   Melton,D., Meadows,A., Clifton,S., Hillier,L., Marra,M., Pape,D.,
            Wylie,T., Martin,J., Blistain,A., Schmitt,A., Theising,B.,
            Ritter,E., Ronko,I., Bennett,J., Cardenas,M., Gibbons,M.,
            McCann,R., Cole,R., Tsagareishvili,R., Williams,T., Jackson,Y. and
            Bowers,Y.
  TITLE     WashU-Harvard Pancreas EST Project
  JOURNAL   Unpublished (2000)
COMMENT     Other_ESTs: ie57a02.y1
            Contact: Douglas Melton, Klaus H. Kaestner, & Hiroshi Inoue
            Endocrine Pancreas Consortium
            Harvard University, Howard Hughes Medical Institute
            Dept of Molecular and Cellular Biology, 7 Divinity Ave, Cambridge,
            MA 02138
            Tel: 617-495-1812
            Fax: 617-495-8557
            Email: dmelton@biohp.harvard.edu
            This read is a 3' RESEQUENCE of a previously sequenced pancreas
            clone
            This resequenced clone has not previously been sequenced on this
            end, resequencing from this end represents new data
            Seq primer: -40UP from Gibco
            High quality sequence stop: 584.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
                     /clone="IMAGE:5670818"
                     /sex="Both"
                     /tissue_type="Islets of Langerhans"
                     /dev_stage="Adult"
                     /lab_host="DH10B"
                     /clone_lib="Melton Normalized Human Islet 4 N4-HIS 1"
                     /note="Organ: Pancreas; Vector: pSPORT1; Site_1: Not 1;
                     Site_2: Sal 1; Starting library constructed using
                     SuperScript Plasmid Library kit  (Life Technologies). cDNA
                     made by oligo-dT priming. Size-selected by  column
                     fractionation; average insert size 1.08 kb. Library was
                     amplified  once on solid support and plasmid DNA from
                     library was prepared. The  library DNA was normalized by
                     method #4 from Bonaldo, Lennon, and Soares  1996 Genome
                     Research 6:791-806; 0.5 microgram single-stranded library
                     plasmid DNA was mixed with 5 micrograms PCR product
                     representing library  inserts and hybridized to an Ecot of
                     20. Single-stranded (unhybridized)  plasmids were isolated
                     by hydroxyapatite chromatography and used to make  this
                     library."
ORIGIN

Alignment Scores:
```

```
Pred. No.:              3.77e-69        Length:         598
Score:                  695.00          Matches:        130
Percent Similarity:     99.24%          Conservative:   0
Best Local Similarity:  99.24%          Mismatches:     1
Query Match:            56.00%          Indels:         0
DB:                     7               Gaps:           0

US-09-914-053A-5 (1-235) x CK903430 (1-598)

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||| |||||||||||||||||||||||||||||||||||||||||||||||||||
Db        598 TGCTGGAAATTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 539

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        538 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 479

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        478 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 419

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 359

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 GTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 299

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 239

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||
Db        238 CTACTATGTGAGAGGATCCAACGGATCAATAGA 206

RESULT 13
CK476300
LOCUS       CK476300                709 bp    mRNA    linear   EST 14-JAN-2004
DEFINITION  AGENCOURT_17578304 NIH_MGC_232 Rattus norvegicus cDNA clone
            IMAGE:7122446 5', mRNA sequence.
ACCESSION   CK476300
VERSION     CK476300.1  GI:40820398
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 709)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15008  row: n  column: 12
            High quality sequence stop: 710.
FEATURES             Location/Qualifiers
     source          1. .709
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7122446"
                     /tissue_type="lung, pooled"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_232"
                     /note="Organ: lung; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from pooled lung tissue from a
                     mix of male and female animals at 8 wk old. Tissues were
                     snap-frozen and kept at -80C for two days before RNA
                     extraction and purification (Tri-reagent method). cDNA was
                     primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
                     resulted in an average insert size of 2.3 kb. This primary
                     library is normalized (non-normalized primary library is
                     NIH_MGC_231) and was constructed by Express Genomics
                     (Frederick, MD). Note: this is a NIH_MGC library."
ORIGIN

Alignment Scores:
Pred. No.:              4.87e-69        Length:         709
Score:                  695.00          Matches:        131
Percent Similarity:     97.78%          Conservative:   1
Best Local Similarity:  97.04%          Mismatches:     3
Query Match:            56.00%          Indels:         0
DB:                     7               Gaps:           0

US-09-914-053A-5 (1-235) x CK476300 (1-709)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        304 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACACGACGAGAAAAGAAAT 363

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        364 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 423

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        424 AAGGCTGGGGAGGACCGGGCCATCCTGCTTGGACTGGCCATGATGGTGTGCTCCATCATG 483

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        484 ATGTACTTCCTACTGGGAATCACACTGCTGCGCTCGTACATGCAGAGTGTATGGACAGAA 543

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::|||||   |||||||||   ||||||||||||||||||||||||||||||||||
Db        544 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACATTTAACTGTTCCTTCAGC 603

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        604 TGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAACCTG 663

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThr 135
              |||||||||||||||||||||||||||||||||||||||||||||
Db        664 ACATCTTCTGGGGAGAAGCTCCTCCTCTACCACACAGAAGAGACC 708

RESULT 14
BX729097
LOCUS       BX729097                852 bp    mRNA    linear   EST 18-NOV-2003
DEFINITION  BX729097 XGC-tadpole Xenopus tropicalis cDNA clone TTpA078h06 5',
            mRNA sequence.
ACCESSION   BX729097
VERSION     BX729097.1  GI:38401838
KEYWORDS    EST.
SOURCE      Xenopus tropicalis (western clawed frog)
  ORGANISM  Xenopus tropicalis
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidea; Pipidae;
            Xenopodinae; Xenopus; Silurana.
REFERENCE   1  (bases 1 to 852).
  AUTHORS   Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
  TITLE     Sanger Xenopus tropicalis EST project 2001 (11_2003)
  JOURNAL   Unpublished (2003)
```

```
COMMENT     Contact: Croning MDR
            Sanger Institute
            Hinxton, Cambridgeshire, CB10 1SA, UK
            Email: trop@sanger.ac.uk
            Sanger Xenopus tropicalis EST project 2001
            TROPICALIS_SEQUENCE_ID: TTpA078h06.p1kSP6
            Sequencing primer: SP6
            This sequence is from a Xenopus Gene Collection (XGC) library
            constructed by Nigel Garrett.
            cDNA was oligo dT primed from 5ug of poly A+ RNA from tadpole
            embryos. EcoRI-NotI cut cDNA was then ligated into pCS107 with
            EcoRI at the 5' end and NotI at the 3' end.
            Vector: pCS107; Site_1: EcoRI; Site_2: NotI
            Host: Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .852
                     /organism="Xenopus tropicalis"
                     /mol_type="mRNA"
                     /db_xref="taxon:8364"
                     /clone="TTpA078h06"
                     /dev_stage="tadpole (stage 35-40)"
                     /lab_host="E. coli DH10B"
                     /clone_lib="XGC-tadpole"
                     /note="Vector: pCS107; Site_1: EcoRI; Site_2: NotI; cDNA
                     was oligo dT primed from 5ug of poly A+ RNA from tadpole
                     embryos. EcoRI-NotI cut cDNA was then ligated into pCS107
                     with EcoRI at the 5' end and NotI at the 3' end"
ORIGIN

Alignment Scores:
Pred. No.:                4.1e-68        Length:          852
Score:                    688.00         Matches:         127
Percent Similarity:       95.17%         Conservative:    11
Best Local Similarity:    87.59%         Mismatches:      7
Query Match:              55.44%         Indels:          0
DB:                       5              Gaps:            0

US-09-914-053A-5 (1-235) x BX729097 (1-852)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||:::|||||||||||||||   ||||||:::|||||
Db        416 ATGTTTATTTGGACCAGTGGCCGGTCCTCGTCATCATACAGACCCGATGAAAGAAGAAAT 475

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||:::|||||||||||||||||||||||||||||||||||||||||||
Db        476 TTCTACCAAAAAATCAAAGATCATGATCTTCTGGACAAAAGGAAAACTGTGACGGCACTA 535

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        536 AAAGCAGGAGAAGACAGAGCTATACTTCTGGGACTTGCAATGATGGTGTGCTCCATTATG 595

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        596 ATGTATTTTCTCCTAGGAATAACATTGCTGCGATCATACATGCAGAGCGTATGGACAGAA 655

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::|||||||||||:::|||||||||||||||||||||||||||||||||||||||
Db        656 GAGACACAATGCACATTAATGAATGCATCTATAACAGAAACCTTCAACTGCTCCTTCAGT 715

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||   :::|||||||||||||||||||||||||||||||||||
Db        716 TGTGGTCCAGATTGCTGGNAAATCTCTCAGTACCCCTGTCTACAGGTTTATGTAAACCTG 775

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              |||||||||:::|||:::|||||||||||||||||||||||:::|||:::|||
Db        776 AATTCTTCAGGACAGAAGGTCCTTCTCTACCACACAGAAGAAACTATGAAAGTGAATTCT 835

Qy        141 LysCysSerTyrIle 145
              :::   |||||||||
Db        836 GAGTNGTCATACATA 850

RESULT 15
CK601161
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```
LOCUS       CK601161                835 bp    mRNA    linear   EST 22-JAN-2004
DEFINITION  AGENCOURT_17898293 NIH_MGC_234 Rattus norvegicus cDNA clone
            IMAGE:7190722 5', mRNA sequence.
ACCESSION   CK601161
VERSION     CK601161.1  GI:41114346
KEYWORDS    EST.
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 835)
  AUTHORS   NIH-MGC http://mgc.nci.nih.gov/.
  TITLE     National Institutes of Health, Mammalian Gene Collection (MGC)
  JOURNAL   Unpublished (1999)
COMMENT     Contact: Daniela S. Gerhard, Ph.D.
            Office of Cancer Genomics
            National Cancer Institute / NIH
            Bldg. 31 Rm10A07 Bethesda, MD 20892
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Howard Jacobs
             cDNA Library Preparation: Express Genomics
             cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
             DNA Sequencing by: Agencourt Bioscience Corporation
             Clone distribution: MGC clone distribution information can be
            found through the I.M.A.G.E. Consortium/LLNL at:
            http://image.llnl.gov
            Plate: LLAM15048  row: k  column: 08
            High quality sequence stop: 681.
FEATURES             Location/Qualifiers
     source          1. .835
                     /organism="Rattus norvegicus"
                     /mol_type="mRNA"
                     /db_xref="taxon:10116"
                     /clone="IMAGE:7190722"
                     /tissue_type="heart, pooled"
                     /lab_host="DH10B TonA"
                     /clone_lib="NIH_MGC_234"
                     /note="Organ: heart; Vector: pExpress-1; Site_1: EcoRV;
                     Site_2: NotI; RNA obtained from pooled heart tissue from a
                     mix of male and female animals at 8 wk old. Tissues were
                     snap-frozen and kept at -80C for two days before RNA
                     extraction and purification (Tri-reagent method). cDNA was
                     primed using oligo-dT primer:
                     5'-pGACTAGTTCTAGATCGCGAGCGGCCGCCC(T)25-3' and cloned into
                     the EcoRV/NotI sites of pExpress-1. Size-selection >1.4kb
                     resulted in an average insert size of 2.2 kb. This primary
                     library is normalized (non-normalized primary library is
                     NIH_MGC_233) and was constructed by Express Genomics
                     (Frederick, MD). Note: this is a NIH_MGC library."
ORIGIN

Alignment Scores:
Pred. No.:                1.89e-64       Length:          835
Score:                    656.00         Matches:         135
Percent Similarity:       75.54%         Conservative:    4
Best Local Similarity:    73.37%         Mismatches:      21
Query Match:              52.86%         Indels:          24
DB:                       7              Gaps:            4

US-09-914-053A-5 (1-235) x CK601161 (1-835)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        298 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACACGACGAGAAAAGAAAT 357

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        358 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 417

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        418 AAGGCTGGGGAGGACCGGGCCATCCTGCTTGGACTGGCCATGATGGTGTGCTCCATCATG 477
```

```
Qy          61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         478 ATGTACTTCCTACTGGGAATCACACTGCTGCGCTCGTACATGCAGAGTGTATGGACAGAA 537

Qy          81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
               |||:::||||||   |||||||||   ||||||||||||||||||||||||||||||||||||
Db         538 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACATTTAACTGTTCCTTCAGC 597

Qy         101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
               ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         598 TGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAACCTG 657

Qy         121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGlu------GluThrIleLysIle 138
               ||||||||||||||          |||   |||||||||      |||   ||||||:::
Db         658 ACATCTTCTGGGGAGAGCTCCTCTCTA---CACACAGAGAGACATGAGATCATCAAAGTG 714

Qy         139 AsnGlnLysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeu 158
                                                                      |||
Db         715 ------------------------------------------------------CTC 717

Qy         159 ValAsnValValMetGluAsnPheArgLysTyrGlnHisPheSer------CysTyrSer 176
                     :::|||          |||                |||      ||||||
Db         718 TATATCCTAGTGTGGAACACTTTGAGATCATGTCCTAGTCTTTCATCAGACTGCTACGGT 777

Qy         177 AspProGluGly 180
               :::      |||
Db         778 GAGACAGCTGGA 789
```

Search completed: November 7, 2004, 03:20:13
Job time : 2967 secs

GenCore version 5.1.6

OM protein - nucleic search, using frame_plus_p2n model

Run on: November 6, 2004, 23:41:12 ; Search time 3107 Seconds
(without alignments)
3576.788 Million cell updates/sec

Title: US-09-914-053A-5
Perfect score: 1241
Sequence: 1 MSIWTSGRTSSSYRHDEKRN.....MVKLTQYLSLLCERIQRINR 235

Scoring table: BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4526729 seqs, 23644849745 residues

Total number of hits satisfying chosen parameters: 9053458

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:
-MODEL=frame+_p2n.model -DEV=xlp
-Q=/cgn2_1/USPTO_spool_p/US09914053/runat_04112004_183921_18221/app_query.fasta_1.391
-DB=GenEmbl -QFMT=fastap -SUFFIX=rge -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US09914053_@CGN_1_1_5600_@runat_04112004_183921_18221 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl:*
1: gb_ba:*
2: gb_htg:*
3: gb_in:*
4: gb_om:*
5: gb_ov:*
6: gb_pat:*
7: gb_ph:*
8: gb_pl:*
9: gb_pr:*
10: gb_ro:*
11: gb_sts:*
12: gb_sy:*
13: gb_un:*
14: gb_vi:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1235	99.5	1075	9	AF099137	AF099137 Homo sapi
2	1235	99.5	1285	9	BC017825	BC017825 Homo sapi
3	1235	99.5	2574	9	AF209747	AF209747 Homo sapi
4	1196	96.4	1062	6	CQ714334	CQ714334 Sequence
5	1186	95.6	708	10	AY062429	AY062429 Mus muscu
6	1186	95.6	2947	10	BC046227	BC046227 Mus muscu
7	1186	95.6	2947	10	BC058957	BC058957 Mus muscu
8	1185	95.5	708	10	AY191836	AY191836 Rattus no
9	1117.5	90.0	1546	5	BX950825	BX950825 Gallus ga
10	1117.5	90.0	1546	5	BX950833	BX950833 Gallus ga
11	1012	81.5	2098	6	BD223084	BD223084 98 human
12	1012	81.5	2098	6	AR243782	AR243782 Sequence
13	821	66.2	487	10	RNO517198	AJ517198 Rattus no
14	510.5	41.1	204899	9	AC117457	AC117457 Homo sapi
15	509	41.0	815	5	CCU67865	U67865 Coturnix co
16	492.5	39.7	191186	2	AC115077	AC115077 Mus muscu
17	492	39.6	826	5	AF077369	AF077369 Gallus ga
18	492	39.6	1290	5	AF420468	AF420468 Gallus ga
19	487.5	39.3	297398	2	AC097578	AC097578 Rattus no
c 20	482.5	38.9	227094	2	AC126508	AC126508 Rattus no
21	481.5	38.8	1246	6	AR212367	AR212367 Sequence
22	478.5	38.6	1022	6	CQ715541	CQ715541 Sequence
23	478	38.5	1111	6	AR212368	AR212368 Sequence
24	477.5	38.5	1225	9	AF204159	AF204159 Homo sapi
25	474.5	38.2	1022	9	AF139471	AF139471 Homo sapi
26	474.5	38.2	1747	9	AF204161	AF204161 Homo sapi
27	474	38.2	952	9	AF214561	AF214561 Homo sapi
28	474	38.2	1160	9	AF170916	AF170916 Homo sapi
29	474	38.2	1311	9	AF204162	AF204162 Homo sapi
30	474	38.2	1488	9	AF160968	AF160968 Homo sapi
31	474	38.2	1620	9	AF204160	AF204160 Homo sapi
32	421	33.9	576	9	AF026002	AF026002 Homo sapi
33	421	33.9	576	9	HSU38907	U38907 Human beta-
34	421	33.9	715	9	AY044441	AY044441 Homo sapi
35	421	33.9	835	9	AY515264	AY515264 Homo sapi
36	421	33.9	1041	9	HSU42600	U42600 Human calci
37	421	33.9	1092	9	HSU61536	U61536 Human potas
38	421	33.9	1106	6	AR016453	AR016453 Sequence
39	421	33.9	1106	6	I45572	I45572 Sequence 3
40	421	33.9	1276	6	CQ726048	CQ726048 Sequence
41	421	33.9	1277	6	AX337509	AX337509 Sequence
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44	418	33.7	1278	10	AF020712	AF020712 Rattus no
45	415	33.4	680	10	MMCAKBETA	AJ001291 Mus muscu

ALIGNMENTS

RESULT 1
AF099137
LOCUS AF099137 1075 bp mRNA linear PRI 06-APR-1999
DEFINITION Homo sapiens MaxiK channel beta 2 subunit (KCNMB2) mRNA, complete cds.
ACCESSION AF099137
VERSION AF099137.1 GI:4566496
KEYWORDS .
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1075)
AUTHORS Wallner,M., Meera,P. and Toro,L.
TITLE Molecular basis of fast inactivation in voltage and Ca2+-activated K+ channels: a transmembrane beta-subunit homolog
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 96 (7), 4137-4142 (1999)
MEDLINE 99199323
PUBMED 10097176
REFERENCE 2 (bases 1 to 1075)
AUTHORS Wallner,M.
TITLE Direct Submission
JOURNAL Submitted (16-OCT-1998) Dept. of Anesthesiology, UCLA, BH-612, CHS Box 951778, Los Angeles, CA 90095-1778, USA
FEATURES Location/Qualifiers
source 1. .1075
/organism="Homo sapiens"
/mol_type="mRNA"

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     CDS             146. .853
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                     channel alpha subunit leads to fast inactivating currents
                     and to an increase in apparent Ca2+ sensitivity"
                     /note="modulatory subunit of the voltage and Ca2+
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                     /codon_start=1
                     /product="MaxiK channel beta 2 subunit"
                     /protein_id="AAD23380.1"
                     /db_xref="GI:4566497"
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                     unclassified site"
     misc_feature    287. .355
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ORIGIN

Alignment Scores:
Pred. No.:                9.98e-126      Length:          1075
Score:                    1235.00        Matches:         234
Percent Similarity:       99.57%         Conservative:    0
Best Local Similarity:    99.57%         Mismatches:      1
Query Match:              99.52%         Indels:          0
DB:                       9              Gaps:            0

US-09-914-053A-5 (1-235) x AF099137 (1-1075)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
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Db        146 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 205

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
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Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
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Db        266 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 325

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
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Db        326 ATGTATTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 385

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
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Db        386 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 445

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
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Db        446 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 505

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
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Db        506 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 565

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
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Db        566 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 625

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
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Db        626 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 685

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
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Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Db        746 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 805

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
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Db        806 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 850

RESULT 2
BC017825
LOCUS       BC017825                1285 bp    mRNA    linear   PRI 29-JUN-2004
DEFINITION  Homo sapiens potassium large conductance calcium-activated channel,
            subfamily M, beta member 2, transcript variant 1, mRNA (cDNA clone
            MGC:22431 IMAGE:4657825), complete cds.
ACCESSION   BC017825
VERSION     BC017825.1  GI:17389593
KEYWORDS    MGC.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 1285)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 1285)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (03-DEC-2001) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: ATCC
            cDNA Library Preparation: CLONTECH Laboratories, Inc.
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Sequencing Group at the Stanford Human Genome
            Center, Stanford University School of Medicine, Stanford, CA  94305
            Web site:       http://www-shgc.stanford.edu
            Contact:  (Dickson, Mark) mcd@paxil.stanford.edu
            Dickson, M., Schmutz, J., Grimwood, J., Rodriquez, A., and Myers,
            R. M.
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          Clone distribution: MGC clone distribution information can be found
          through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
          Series: IRAL Plate: 36 Row: i Column: 8
          This clone was selected for full length sequencing because it
          passed the following selection criteria: matched mRNA gi: 19923319.
FEATURES             Location/Qualifiers
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                     /lab_host="DH10B"
                     /note="Vector: pDNR-LIB"
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                     /db_xref="MIM:605214"
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ORIGIN

Alignment Scores:
Pred. No.:              1.25e-125     Length:          1285
Score:                  1235.00       Matches:         234
Percent Similarity:     99.57%        Conservative:    0
Best Local Similarity:  99.57%        Mismatches:      1
Query Match:            99.52%        Indels:          0
DB:                     9             Gaps:            0

US-09-914-053A-5 (1-235) x BC017825 (1-1285)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
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Db        344 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 403

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
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Db        404 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 463

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
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Db        464 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 523

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
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Db        524 ATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAA 583

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Db        584 GAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAGC 643

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Db        644 TGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTG 703

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
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Db        704 ACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAG 763

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
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Db        764 AAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 823

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
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Db        824 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 883

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
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Db        884 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 943

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
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RESULT 3
AF209747
LOCUS       AF209747               2574 bp    mRNA    linear   PRI 29-FEB-2000
DEFINITION  Homo sapiens large conductance calcium-activated potassium channel
            beta2 subunit (KCNMB2) mRNA, complete cds.
ACCESSION   AF209747
VERSION     AF209747.1  GI:7108972
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2574)
  AUTHORS   Brenner,R., Jegla,T.J., Wickenden,A., Liu,Y. and Aldrich,R.W.
  TITLE     Cloning and functional characterization of novel large conductance
            calcium-activated potassium channel beta subunits, hKCNMB3 and
            hKCNMB4
  JOURNAL   J. Biol. Chem. 275 (9), 6453-6461 (2000)
  MEDLINE   20158960
   PUBMED   10692449
REFERENCE   2  (bases 1 to 2574)
  AUTHORS   Brenner,R., Jegla,T.J., Wickenden,A., Liu,Y. and Aldrich,R.W.
  TITLE     Direct Submission
  JOURNAL   Submitted (30-NOV-1999) Molecular and Cell Physiology, Howard
            Hughes Medical Institute, Stanford School of Medicine, Beckman
            B173, Stanford, CA 94305, USA
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ORIGIN

Alignment Scores:
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Pred. No.:                2.99e-125       Length:          2574
Score:                    1235.00         Matches:         234
Percent Similarity:       99.57%          Conservative:    0
Best Local Similarity:    99.57%          Mismatches:      1
Query Match:              99.52%          Indels:          0
DB:                       9               Gaps:            0

US-09-914-053A-5 (1-235) x AF209747 (1-2574)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
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Db        353 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 412

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
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Db        413 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACAGTCACAGCACTG 472

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
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Db        473 AAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATG 532

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
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Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
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Db        893 AACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 952

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Db        953 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 1012

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
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Db       1013 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 1057

RESULT 4
CQ714334
LOCUS       CQ714334                1062 bp    DNA     linear   PAT 03-FEB-2004
DEFINITION  Sequence 268 from Patent WO02068579.
ACCESSION   CQ714334
VERSION     CQ714334.1  GI:42275191
KEYWORDS    .
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
  AUTHORS   Venter,C.J., Adams,M.C., Li,P.W. and Myers,E.W.
  TITLE     Kits, such as nucleic acid arrays, comprising a majority of
            humanexons or transcripts, for detecting expression and other uses
            thereof
  JOURNAL   Patent: WO 02068579-A 268 06-SEP-2002;
            PE Corporation (NY) (US)
FEATURES             Location/Qualifiers
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                     /mol_type="unassigned DNA"
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ORIGIN

Alignment Scores:
Pred. No.:                1.88e-121       Length:          1062
Score:                    1196.00         Matches:         234
Percent Similarity:       98.32%          Conservative:    0
Best Local Similarity:    98.32%          Mismatches:      1
Query Match:              96.37%          Indels:          3
DB:                       6               Gaps:            0

US-09-914-053A-5 (1-235) x CQ714334 (1-1062)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||  ||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        147 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTATAGACATGATGAAAAAAGAAAT 206

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeu-AspLysArgLysThrValThrAlaLe 40
              ||||||||||||||||||||||||||||||| ||||||||||||||||||||||||||||
Db        207 ATTTACCAGAAAATCAGGGACCATGACCTCCTGGGACAAAAGGAAAACAGTCACAGCACT 266

Qy         40 uLysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMe 60
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        267 GAAGGCAGGAGAGGACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCAT 326

Qy         60 tMetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGl 80
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        327 GATGTATTTTCTGCTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGA 386

Qy         80 uGluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSe 100
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        387 AGAGTCTCAATGCACCTTGCTGAATGCGTCCATCACGGAAACATTTAACTGCTCCTTCAG 446

Qy        100 rCysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLe 120
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        447 CTGTGGTCCAGACTGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCT 506

Qy        120 uThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGl 140
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        507 GACTTCTTCCGGGGAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCA 566

Qy        140 nLysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAs 160
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        567 GAAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAA 626

Qy        160 nValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGl 180
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        627 TGTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGG 686

Qy        180 yAsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLe 200
              |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        687 AAACCAGAAGAGTGTTATCCTAACCAAACTCTACAGTTCCAACGTGCTGTTCCATTCACT 746

Qy        200 uPheTrpProThrCysMetMetAla-GlyGlyValAlaIleValAlaMetValLysLeuT 220
              |||||||||||||||||||||||| |||||||||||||||||||||||||||||||||||
Db        747 CTTCTGGCCAACCTGTATGATGGCTGGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTA 806

Qy        220 hrGlnTyrLeuSerLeuLeuCysGluArgIleGlnArg-IleAsnArg 235
              |||||||||||||||||||||||||||||||||||||| ||||||||
Db        807 CACAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGGATCAATAGG 854

RESULT 5
AY062429
LOCUS       AY062429                708 bp    mRNA    linear   ROD 12-DEC-2001
DEFINITION  Mus musculus large conductance calcium-activated K channel beta2
            subunit mRNA, complete cds.
ACCESSION   AY062429
```

```
VERSION     AY062429.1  GI:17644138
KEYWORDS    .
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Garcia-Valdes,J., Eghbali,M., Stefani,E. and Toro,L.
  TITLE     Mouse kcnmb2 subunit of the large conductance calcium-activated K
            channel (MaxiK, BK)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 708)
  AUTHORS   Garcia-Valdes,J., Eghbali,M., Stefani,E. and Toro,L.
  TITLE     Direct Submission
  JOURNAL   Submitted (14-NOV-2001) Anesthesiology, UCLA, PO Box 957115,
            BH-509A CHS, Los Angeles, CA 90095-7115, USA
FEATURES             Location/Qualifiers
     source          1. .708
                     /organism="Mus musculus"
                     /mol_type="mRNA"
                     /strain="C57BL/6"
                     /db_xref="taxon:10090"
                     /tissue_type="kidney"
                     /dev_stage="fetus"
     CDS             1. .708
                     /note="inactivating subunit; MaxiK; BK; kcnmb2"
                     /codon_start=1
                     /product="large conductance calcium-activated K channel
                     beta2 subunit"
                     /protein_id="AAL38982.1"
                     /db_xref="GI:17644139"
                     /translation="MFIWTSGRTSSSYRQDEKRNIYQKIRDHDLLDKRKTVTALKAGE
                     DRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEEAQCALLNVSITETFNCSFSCG
                     PDCWKLSQYPCLQVYVNLTSSGERLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVS
                     VVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVK
                     LTQYLSLLCERIQRINR"
ORIGIN

Alignment Scores:
Pred. No.:                1.41e-120      Length:          708
Score:                    1186.00        Matches:         223
Percent Similarity:       97.45%         Conservative:    6
Best Local Similarity:    94.89%         Mismatches:      6
Query Match:              95.57%         Indels:          0
DB:                       10             Gaps:            0

US-09-914-053A-5 (1-235) x AY062429 (1-708)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db          1 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 60

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 120

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 180

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 240

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::||||||   ||||||||   ||||||||||||||||||||||||||||||||||
Db        241 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 300

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 360

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||:::|||||||||||||||||||||||||||||:::|||||||||||
Db        361 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 420

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||||   ||||||||||||||||||||||||||||:::
Db        421 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 480

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||:::::|||||||||   ||||||||||||||||||||
Db        481 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 540

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 600

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        601 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 660

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 705

RESULT 6
BC046227
LOCUS       BC046227               2947 bp    mRNA    linear   ROD 30-JUN-2004
DEFINITION  Mus musculus potassium large conductance calcium-activated channel,
            subfamily M, beta member 2, mRNA (cDNA clone MGC:57945
            IMAGE:5703879), complete cds.
ACCESSION   BC046227
VERSION     BC046227.1  GI:28279339
KEYWORDS    MGC.
SOURCE      Mus musculus (house mouse)
  ORGANISM  Mus musculus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE   1  (bases 1 to 2947)
  AUTHORS   Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G.,
            Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D.,
            Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K.,
            Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F.,
            Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L.,
            Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L.,
            Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S.,
            Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J.,
            Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J.,
            McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S.,
            Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W.,
            Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A.,
            Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S.,
            Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y.,
            Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D.,
            Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M.,
            Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E.,
            Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
  TITLE     Generation and initial analysis of more than 15,000 full-length
            human and mouse cDNA sequences
  JOURNAL   Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
   PUBMED   12477932
REFERENCE   2  (bases 1 to 2947)
  AUTHORS   Strausberg,R.
  TITLE     Direct Submission
  JOURNAL   Submitted (31-JAN-2003) National Institutes of Health, Mammalian
            Gene Collection (MGC), Cancer Genomics Office, National Cancer
            Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,
            USA
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: University of Iowa, Dr. M. Bento Soares and Dr.
```

Thomas L. Casavant.
Web site: http://genome.uiowa.edu
Contact: bento-soares@uiowa.edu; tom-casavant@uiowa.edu
Bonaldo,M.F., Akabogu,I., Bair,T., Bair,J., Crouch,K., Davis,A., Fishler,K., Keppel,C., Kucaba,T., Lebeck,M., Melo,A., Schaefer,K., Scheetz,T., Smith,C., Snir,E., Tack,D., Trout,K., Walters,J., Casavant,T., Soares,M.B.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
Series: Plate: Row: Column: 0
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 21312299.

FEATURES Location/Qualifiers
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/mol_type="mRNA"
/strain="C57BL/6"
/db_xref="taxon:10090"
/clone="MGC:57945 IMAGE:5703879"
/tissue_type="Brain, mouse 15.5 dpc"
/clone_lib="NIH_BMAP_EW0"
/lab_host="DH10B"
/note="Vector: pYX-ASC"
gene 1. .2947
/gene="Kcnmb2"
/note="synonym: MGC57945"
/db_xref="LocusID:72413"
/db_xref="MGI:1919663"
CDS 391. .1098
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/product="potassium large conductance calcium-activated channel, subfamily M, beta member 2"
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/db_xref="LocusID:72413"
/db_xref="MGI:1919663"
/translation="MFIWTSGRTSSSYRQDEKRNIYQKIRDHDLLDKRKTVTALKAGE
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PDCWKLSQYPCLQVYVNLTSSGERLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVS
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LTQYLSLLCERIQRINR"

ORIGIN

Alignment Scores:

Pred. No.:	8.5e-120	Length:	2947
Score:	1186.00	Matches:	223
Percent Similarity:	97.45%	Conservative:	6
Best Local Similarity:	94.89%	Mismatches:	6
Query Match:	95.57%	Indels:	0
DB:	10	Gaps:	0

US-09-914-053A-5 (1-235) x BC046227 (1-2947)

```
Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              ||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        391 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 450

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 510

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 570

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 630

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::||||||   |||||||||   ||||||||||||||||||||||||||||||||
Db        631 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 690

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
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Db        691 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 750

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||:::|||||||||||||||||||||||||||:::|||||||||||||
Db        751 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 810

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              |||||||||||||||||||||||||  |||||||||||||||||||||||||||:::
Db        811 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 870

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
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Db        871 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 930

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 990

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1051 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 1095
```

RESULT 7
BC058957
LOCUS BC058957 2947 bp mRNA linear ROD 30-JUN-2004
DEFINITION Mus musculus potassium large conductance calcium-activated channel, subfamily M, beta member 2, mRNA (cDNA clone MGC:66775 IMAGE:5703879), complete cds.
ACCESSION BC058957
VERSION BC058957.1 GI:37589334
KEYWORDS MGC.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE 1 (bases 1 to 2947)
AUTHORS Strausberg,R.L., Feingold,E.A., Grouse,L.H., Derge,J.G., Klausner,R.D., Collins,F.S., Wagner,L., Shenmen,C.M., Schuler,G.D., Altschul,S.F., Zeeberg,B., Buetow,K.H., Schaefer,C.F., Bhat,N.K., Hopkins,R.F., Jordan,H., Moore,T., Max,S.I., Wang,J., Hsieh,F., Diatchenko,L., Marusina,K., Farmer,A.A., Rubin,G.M., Hong,L., Stapleton,M., Soares,M.B., Bonaldo,M.F., Casavant,T.L., Scheetz,T.E., Brownstein,M.J., Usdin,T.B., Toshiyuki,S., Carninci,P., Prange,C., Raha,S.S., Loquellano,N.A., Peters,G.J., Abramson,R.D., Mullahy,S.J., Bosak,S.A., McEwan,P.J., McKernan,K.J., Malek,J.A., Gunaratne,P.H., Richards,S., Worley,K.C., Hale,S., Garcia,A.M., Gay,L.J., Hulyk,S.W., Villalon,D.K., Muzny,D.M., Sodergren,E.J., Lu,X., Gibbs,R.A., Fahey,J., Helton,E., Ketteman,M., Madan,A., Rodrigues,S., Sanchez,A., Whiting,M., Madan,A., Young,A.C., Shevchenko,Y., Bouffard,G.G., Blakesley,R.W., Touchman,J.W., Green,E.D., Dickson,M.C., Rodriguez,A.C., Grimwood,J., Schmutz,J., Myers,R.M., Butterfield,Y.S., Krzywinski,M.I., Skalska,U., Smailus,D.E., Schnerch,A., Schein,J.E., Jones,S.J. and Marra,M.A.
TITLE Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)
PUBMED 12477932
REFERENCE 2 (bases 1 to 2947)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (01-OCT-2003) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA

```
  REMARK    NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT     Contact: MGC help desk
            Email: cgapbs-r@mail.nih.gov
            Tissue Procurement: Dr. Jim Lin, University of Iowa
            cDNA Library Preparation: M. Bento Soares, University of Iowa
            cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
            DNA Sequencing by: Genome Sequence Centre,
            BC Cancer Agency, Vancouver, BC, Canada
            info@bcgsc.bc.ca
            Steve Jones, Sarah Barber, Mabel Brown-John, Yaron Butterfield,
            Andy Chan, Steve S. Chand, William Chow, Alison Cloutier, Ruth
            Featherstone, Malachi Griffith, Obi Griffith, Ran Guin, Nancy Liao,
            Kim MacDonald, Amara Masson, Mike R. Mayo, Josh Moran, Ryan Morin,
            Teika Olson, Diana Palmquist, Anca Petrescu, Anna Liisa Prahbu,
            Parvaneh Saeedi, JR Santos, Angelique Schnerch, Ursula Skalska,
            Duane Smailus, Jeff Stott, Miranda Tsai, George Yang, Jacquie
            Schein, Asim Siddiqui, Rob Holt, Marco Marra.

            Clone distribution: MGC clone distribution information can be found
            through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov
            Series: IRAK Plate: 124 Row: i Column: 16
            This clone was selected for full length sequencing because it
            passed the following selection criteria: matched mRNA gi: 21312299.
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                      /db_xref="LocusID:72413"
                      /db_xref="MGI:1919663"
     CDS              391. .1098
                      /gene="Kcnmb2"
                      /codon_start=1
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                      channel, subfamily M, beta member 2"
                      /protein_id="AAH58957.1"
                      /db_xref="GI:37589335"
                      /db_xref="LocusID:72413"
                      /db_xref="MGI:1919663"
                      /translation="MFIWTSGRTSSSYRQDEKRNIYQKIRDHDLLDKRKTVTALKAGE
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                      PDCWKLSQYPCLQVYVNLTSSGERLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVS
                      VVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVK
                      LTQYLSLLCERIQRINR"
ORIGIN

Alignment Scores:
Pred. No.:                8.5e-120        Length:          2947
Score:                    1186.00         Matches:         223
Percent Similarity:       97.45%          Conservative:    6
Best Local Similarity:    94.89%          Mismatches:      6
Query Match:              95.57%          Indels:          0
DB:                       10              Gaps:            0

US-09-914-053A-5 (1-235) x BC058957 (1-2947)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||||||||||||||||||||||   ||||||||||||||||
Db        391 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACAGGACGAGAAAAGAAAT 450

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        451 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 510

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        511 AAGGCTGGGGAGGACCGGGCCATCCTGCTCGGCCTGGCCATGATGGTGTGCTCCATCATG 570

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        571 ATGTACTTCCTGCTGGGAATCACACTGCTGCGCTCCTACATGCAGAGCGTGTGGACAGAA 630

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::||||||   |||||||||   ||||||||||||||||||||||||||||||||||
Db        631 GAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACGTTTAACTGTTCCTTCAGC 690

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        691 TGTGGGCCCGACTGTTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTGTACGTGAACCTG 750

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||:::||||||||||||||||||||||||||:::|||||||||||||
Db        751 ACATCTTCCGGGGAGAGGCTCCTCCTCTACCACACGGAAGAGACCATGAAGATCAATCAA 810

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              |||||||||||||||||||||||||   |||||||||||||||||||||||||||:::
Db        811 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCTCTCGTGAGT 870

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||||:::::|||||||||   ||||||||||||||||||||
Db        871 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGA 930

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        931 AACCAGAAGAGTGTCATCCTGACCAAACTCTACAGCTCCAATGTGCTGTTCCATTCTCTC 990

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        991 TTCTGGCCAACTTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 1050

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db       1051 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 1095

RESULT 8
AY191836
LOCUS       AY191836                 708 bp    mRNA    linear   ROD 26-FEB-2003
DEFINITION  Rattus norvegicus inactivating beta 2 subunit of large conductance
            Ca2+-activated K+ channel mRNA, complete cds.
ACCESSION   AY191836
VERSION     AY191836.1  GI:28565441
KEYWORDS    .
SOURCE      Rattus norvegicus (Norway rat)
  ORGANISM  Rattus norvegicus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
            Rattus.
REFERENCE   1  (bases 1 to 708)
  AUTHORS   Eghbali,M., Foroughi,S., Toro,L. and Stefani,E.
  TITLE     Rat inactivating beta 2 subunit of large conductance Ca2+-activated
            K+ channel (KCNMB2, rSlo beta 2 subunit)
  JOURNAL   Unpublished
REFERENCE   2  (bases 1 to 708)
  AUTHORS   Eghbali,M., Foroughi,S., Toro,L. and Stefani,E.
  TITLE     Direct Submission
  JOURNAL   Submitted (06-DEC-2002) Anesthesiology, UCLA, PO Box 957115, Room
            BH-509A CHS, Los Angeles, CA 90095-7115, USA
FEATURES              Location/Qualifiers
     source           1. .708
                      /organism="Rattus norvegicus"
                      /mol_type="mRNA"
                      /strain="Sprague-Dawley"
                      /db_xref="taxon:10116"
                      /tissue_type="heart; myometrium"
     CDS              1. .708
                      /note="KCNMB2; rSlo beta 2 subunit"
                      /codon_start=1
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                     /product="inactivating beta 2 subunit of large conductance
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                     PDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVS
                     VVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHSLFWPTCMMAGGVAIVAMVK
                     LTQYLSLLCERIQRINR"
     variation       48
                     /replace="t"
     variation       171
                     /replace="t"
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     variation       231
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ORIGIN

Alignment Scores:
Pred. No.:              1.82e-120       Length:         708
Score:                  1185.00         Matches:        224
Percent Similarity:     97.45%          Conservative:   5
Best Local Similarity:  95.32%          Mismatches:     6
Query Match:            95.49%          Indels:         0
DB:                     10              Gaps:           0

US-09-914-053A-5 (1-235) x AY191836 (1-708)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 ATGTTTATATGGACCAGTGGCCGGACCTCTTCATCTTACAGACACGACGAGAAAAGAAAT 60

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 ATCTACCAGAAAATCAGGGACCATGACCTCCTGGACAAAAGGAAAACTGTGACAGCTCTG 120

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 AAGGCTGGAGAGGACCGGGCCATCCTGCTTGGACTGGCCATGATGGTGTGCTCCATCATG 180

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        181 ATGTACTTCCTACTGGGAATCACACTGCTGCGCTCGTACATGCAGAGTGTATGGACAGAA 240

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
              |||:::|||      |||||||||  ||||||||||||||||||||||||||||||||
Db        241 GAAGCCCAGCGTGCCCTGCTGAATGTGTCAATCACAGAAACATTTAACTGTTCCTTCAGC 300

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        301 TGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAACCTG 360

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
              ||||||||||||||||||||||||||||||||||||||||:::|||||||||||||||||
Db        361 ACATCTTCTGGGGAGAAGCTCCTCCTCTACCACACAGAAGAGACCATGAAGATCAATCAA 420

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              ||||||||||||||||||||||||  ||||||||||||||||||||||||||||||:::
Db        421 AAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCCCTTGTGAGT 480

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
              ||||||||||||||||||||::::::|||||||||  ||||||||||||||||||||||
Db        481 GTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAAGGG 540

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        541 AACCAAAAGAGCGTCATCCTGACCAAACTCTATAGCTCCAATGTGCTGTTCCATTCTCTC 600

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||

Db        601 TTCTGGCCAACGTGTATGATGGCTGGGGGTGTGGCAATCGTTGCTATGGTGAAACTAACT 660

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db        661 CAGTACCTCTCCCTGCTTTGTGAGAGGATCCAACGGATCAACAGA 705

RESULT 9
BX950825
LOCUS       BX950825               1546 bp    mRNA    linear   VRT 17-FEB-2004
DEFINITION  Gallus gallus finished cDNA, clone ChEST48b4.
ACCESSION   BX950825
VERSION     BX950825.1  GI:42600510
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
            Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
            Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
            Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
            Tickle,C. and Wilson,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (16-FEB-2004) Sanger Institute, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
COMMENT     BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
            sequencing project.
            This sequence is from the
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
            from a library constructed by Elizabeth Bosch. cDNA was prepared
            from RNA extracted from whole embryo, normalised, and poly
            A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector.
            Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host:
            Escherichia coli DH10B.
FEATURES             Location/Qualifiers
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                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
                     /db_xref="taxon:9031"
                     /clone="ChEST48b4"
                     /clone_lib="CSEQCHN04"
                     /dev_stage="stage 10"
ORIGIN

Alignment Scores:
Pred. No.:              1.25e-112       Length:         1546
Score:                  1117.50         Matches:        210
Percent Similarity:     94.47%          Conservative:   12
Best Local Similarity:  89.36%          Mismatches:     6
Query Match:            90.05%          Indels:         7
DB:                     5               Gaps:           1

US-09-914-053A-5 (1-235) x BX950825 (1-1546)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
              |||   |||||||||||||||||:::|||:::||||||||||||||||||||
Db        144 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 197

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
                                 ||||||||||||||||||||||||||||||||||||||
Db        198 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 242

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        243 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 302

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        303 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 362
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Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
Db        363 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 422

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
Db        423 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 482

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
Db        483 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 542

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
Db        543 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 602

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
Db        603 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 662

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
Db        663 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 722

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
Db        723 TTCTGGCCCACGTGCATGATGATCGGCGGCGTTGCCATTGTTGCGATGGTAAAGCTGACT 782

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
Db        783 CAATACCTTTCTCTCCTCTGCGAGAGAATCCAAAGGATCAACAGA 827
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RESULT 10
BX950833
LOCUS       BX950833               1546 bp    mRNA    linear   VRT 30-MAR-2004
DEFINITION  Gallus gallus finished cDNA, clone ChEST43b24.
ACCESSION   BX950833
VERSION     BX950833.2  GI:46019324
KEYWORDS    .
SOURCE      Gallus gallus (chicken)
  ORGANISM  Gallus gallus
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Gallus.
REFERENCE   1  (bases 1 to 1546)
  AUTHORS   Boardman,P.E., Bonfield,J.K., Brown,W.R.A., Carder,C., Chalk,S.E.,
            Croning,M.D.R., Davies,R.M., Francis,M.D., Grafham,D.V.,
            Hubbard,S.J., Humphray,S.J., Hunt,P.J., Maddison,M., McLaren,S.R.,
            Niblett,D., Overton,I.M., Rogers,J., Scott,C.E., Taylor,R.G.,
            Tickle,C. and Wilson,S.A.
  TITLE     Direct Submission
  JOURNAL   Submitted (29-MAR-2004) Sanger Institute, Hinxton, Cambridgeshire,
            CB10 1SA, UK. E-mail enquiries: chickest@bms.umist.ac.uk
COMMENT     On Apr 1, 2004 this sequence version replaced gi:42600518.
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST Gallus gallus cDNA
            sequencing project.
            This sequence is from the
            BBSRC/Dundee/Nottingham/Sanger/Sheffield/UMIST cDNA collection,
            from a library constructed by Elizabeth Bosch. cDNA was prepared
            from RNA extracted from whole embryo, normalised, and poly
            A-trimmed. EcoRI-NotI cut cDNA was then ligated into the vector.
            Vector: pBluescript II KS(+); Site_1: EcoRI; Site_2: NotI Host:
            Escherichia coli DH10B.
FEATURES             Location/Qualifiers
     source          1. .1546
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                     /mol_type="mRNA"
                     /strain="White Leghorn, Hisex"
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                     /clone="ChEST43b24"
                     /clone_lib="CSEQCHN04"
                     /dev_stage="stage 10"
ORIGIN
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Alignment Scores:
Pred. No.:                1.25e-112      Length:          1546
Score:                    1117.50        Matches:         210
Percent Similarity:       94.47%         Conservative:    12
Best Local Similarity:    89.36%         Mismatches:      6
Query Match:              90.05%         Indels:          7
DB:                       5              Gaps:            1

US-09-914-053A-5 (1-235) x BX950833 (1-1546)

Qy          1 MetSerIleTrpThrSerGlyArgThrSerSerSerTyrArgHisAspGluLysArgAsn 20
Db        144 ATGTTTATTTGGACCAGTGGCCGGAGCTCTACATCTTACAGACACGATGAGAAA------ 197

Qy         21 IleTyrGlnLysIleArgAspHisAspLeuLeuAspLysArgLysThrValThrAlaLeu 40
Db        198 --------------AGGGATCACGATCTACTGGACAAAAGGAAAACAGTCACAGCCCTA 242

Qy         41 LysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMet 60
Db        243 AAAGCTGGAGAAGACCGGGCCATACTCCTCGGGCTGGCCATGATGGTGTGCTCTATCATG 302

Qy         61 MetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGlu 80
Db        303 ATGTACTTTCTCCTGGGAATCACCCTGCTGCGGTCCTACATGCAGAGCGTCTGGACAGAA 362

Qy         81 GluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSer 100
Db        363 GAGGCTCAGTGCTCGCTTCTCAACGCATCCATCACCGAAACCTTCAACTGCTCGTTTAGC 422

Qy        101 CysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeu 120
Db        423 TGCGGCCCAGACTGCTGGAAAATCTCTCAGTACCCCTGCCTGCAGGTGTACGTCAATCTC 482

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
Db        483 ACTTCTTCTGGCCAGAAGCTTCTGCTCTACCACACCGAAGAAACAATGAAAATTAATTCT 542

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
Db        543 GAGTGTTCGTACATACCCAAGTGTGGCAAGAATTACGAGGAATCCATGTCAATGGTGAAC 602

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
Db        603 GTTGTGATGGAAAACTTCCGAAAGTATCAACGCTTCTCCTGCTTCTATGATCCTGAGGGC 662

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
Db        663 ACTCAGAAGAACGTGATATTGACCAAACTGTACAGCTCCAACGTGCTGTTCCACTCGCTC 722

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
Db        723 TTCTGGCCCACGTGCATGATGATCGGCGGCGTTGCCATTGTTGCGATGGTAAAGCTGACT 782

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
Db        783 CAATACCTTTCTCTCCTCTGCGAGAGAATCCAAAGGATCAACAGA 827
```

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RESULT 11
BD223084
LOCUS       BD223084               2098 bp    DNA     linear   PAT 17-JUL-2003
DEFINITION  98 human secretory proteins.
ACCESSION   BD223084
VERSION     BD223084.1  GI:33032854
KEYWORDS    JP 2002521055-A/19.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Komatsoulis,G.A., Rosen,C.A., Ruben,S.M., Duan,R., Moore,P.A.,
            Shi,Y., Lafleur,D., Wei,Y.F., Ni,J., Florence,K.A., Young,P.E.,
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            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H.S. and
            Mucenski,M.
  TITLE     98 human secretory proteins
  JOURNAL   Patent: JP 2002521055-A 19 16-JUL-2002;
            HUMAN GENOME SCIENCES INC
COMMENT     OS   Homo sapiens (human)
            PN   JP 2002521055-A/19
            PD   16-JUL-2002
            PF   29-JUL-1999 JP 2000562480
            PR   30-JUL-1998 US    60/094657,05-AUG-1998 US    60/095486 PR
            06-AUG-1998 US    60/095455,06-AUG-1998 US    60/095454 PR
            12-AUG-1998 US    60/096319
            PI   GEORGE A KOMATSOULIS,CRAIG A ROSEN,STEVEN
            M RUBEN,ROXANNE DUAN,
            PI   PAUL A MOORE,YANGGU SHI,DAVID LAFLEUR,YING FEI WEI,JIAN NI, PI
              KIMBERLY A FLORENCE,PAUL E YOUNG,LAURIE A BREWER,DANIEL R  PI
            SOPPET,
            PI   GREGORY A ENDRESS,REINHARD EBNER,HENRIK S OLSEN,MICHAEL  PI
            MUCENSKI
            PC   C12N15/09,A61K31/713,A61K38/00,A61K48/00,C07K14/47,C07K16/18,
            PC   C12N1/15,
            PC
            C12N1/19,C12N1/21,C12N5/10,C12P21/02,C12P21/08,C12Q1/68,G01N33/ PC
             15,
            PC
            G01N33/50,G01N33/53//A61P1/18,A61P5/02,A61P5/06,A61P5/14,A61P9/ PC
             10,
            PC   A61P11/06,A61P17/06,A61P19/02,A61P25/02,A61P25/14,A61P25/16,
            PC   A61P25/24,
            PC   A61P25/28,A61P27/02,A61P29/00,A61P31/18,A61P35/02,C12N15/00,
            PC   C12N5/00,
            PC   A61K37/02
            CC   98 human secretory proteins
            FH   Key             Location/Qualifiers
            FT   source          1. .2098
            FT                   /organism='Homo sapiens (human)'.
FEATURES             Location/Qualifiers
     source          1. .2098
                     /organism="Homo sapiens"
                     /mol_type="genomic DNA"
                     /db_xref="taxon:9606"
ORIGIN

Alignment Scores:
Pred. No.:              7.01e-101       Length:         2098
Score:                  1012.00         Matches:        191
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            81.55%          Indels:         0
DB:                     6               Gaps:           0

US-09-914-053A-5 (1-235) x BD223084 (1-2098)

Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309

Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
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Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
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Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582

RESULT 12
AR243782
LOCUS       AR243782               2098 bp    DNA     linear   PAT 20-DEC-2002
DEFINITION  Sequence 20 from patent US 6476195.
ACCESSION   AR243782
VERSION     AR243782.1  GI:27291275
KEYWORDS    .
SOURCE      Unknown.
  ORGANISM  Unknown.
            Unclassified.
REFERENCE   1  (bases 1 to 2098)
  AUTHORS   Komatsoulis,G., Rosen,C.A., Ruben,S.M., Duan,R.D., Moore,P.A.,
            Shi,Y., LaFleur,D.W., Wei,Y.-F., Ni,J., Florence,K.A., Young,P.,
            Brewer,L.A., Soppet,D.R., Endress,G.A., Ebner,R., Olsen,H. and
            Mucenski,M.
  TITLE     Secreted protein HNFGF20
  JOURNAL   Patent: US 6476195-A 20 05-NOV-2002;
FEATURES             Location/Qualifiers
     source          1. .2098
                     /organism="unknown"
                     /mol_type="genomic DNA"
ORIGIN

Alignment Scores:
Pred. No.:              7.01e-101       Length:         2098
Score:                  1012.00         Matches:        191
Percent Similarity:     100.00%         Conservative:   0
Best Local Similarity:  100.00%         Mismatches:     0
Query Match:            81.55%          Indels:         0
DB:                     6               Gaps:           0

US-09-914-053A-5 (1-235) x AR243782 (1-2098)

Qy         45 AspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPheLeu 64
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         10 GACCGAGCTATTCTCCTGGGACTGGCTATGATGGTGTGCTCCATCATGATGTATTTTCTG 69

Qy         65 LeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCys 84
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         70 CTGGGAATCACACTCCTGCGCTCATACATGCAGAGCGTGTGGACCGAAGAGTCTCAATGC 129

Qy         85 ThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp 104
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        130 ACCTTGCTGAATGCGTCCATCACGGAAACATTTAATTGCTCCTTCAGCTGTGGTCCAGAC 189

Qy        105 CysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsnLeuThrSerSerGly 124
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        190 TGCTGGAAACTTTCTCAGTACCCCTGCCTCCAGGTGTACGTTAACCTGACTTCTTCCGGG 249

Qy        125 GluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGlnLysCysSerTyr 144
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        250 GAAAAGCTCCTCCTCTACCACACAGAAGAGACAATAAAAATCAATCAGAAGTGCTCCTAT 309
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Qy        145 IleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsnValValMetGlu 164
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        310 ATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAATGTTGTCATGGAA 369

Qy        165 AsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGlyAsnGlnLysSer 184
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        370 AACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGAAACCAGAAGAGT 429

Qy        185 ValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeuPheTrpProThr 204
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        430 GTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTCTTCTGGCCAACC 489

Qy        205 CysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThrGlnTyrLeuSer 224
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        490 TGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACACAGTACCTCTCC 549

Qy        225 LeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||
Db        550 CTACTATGTGAGAGGATCCAACGGATCAATAGA 582
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RESULT 13
RNO517198
LOCUS RNO517198 487 bp mRNA linear ROD 15-DEC-2002
DEFINITION Rattus norvegicus partial mRNA for calcium-activated potassium channel beta 2 subunit (Kcnmb2 gene).
ACCESSION AJ517198
VERSION AJ517198.1 GI:26801163
KEYWORDS calcium-activated potassium channel beta 2 subunit; Kcnmb2 gene.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
REFERENCE 1
AUTHORS Langer,P., Grunder,S. and Rusch,A.
TITLE Expression of Ca2+-activated BK channel mRNA and its splice variants in the rat cochlea
JOURNAL J. Comp. Neurol. 455 (2), 198-209 (2003)
MEDLINE 22342043
PUBMED 12454985
REFERENCE 2 (bases 1 to 487)
AUTHORS Langer,P.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2002) Langer P., Institute of Physiology II, University of Tuebingen, Gmelinstr. 5, Tuebingen, D-72076, GERMANY
FEATURES Location/Qualifiers
source 1. .487
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/mol_type="mRNA"
/strain="Wistar"
/db_xref="taxon:10116"
/tissue_type="brain"
gene 1. .487
/gene="Kcnmb2"
CDS <1. .>487
/gene="Kcnmb2"
/function="ion channel"
/codon_start=2
/product="calcium-activated potassium channel beta 2 subunit"
/protein_id="CAD56888.1"
/db_xref="GI:26801164"
/db_xref="GOA:Q8CF83"
/db_xref="TrEMBL:Q8CF83"
/translation="LKAGEDRAILLGLAMMVCSIMMYFLLGITLLRSYMQSVWTEEAQCALLNVSITETFNCSFSCGPDCWKLSQYPCLQVYVNLTSSGEKLLLYHTEETMKINQKCSYIPKCGNNFEESMSLVSVVMENFRRHQHFPCYSDPEGNQKSVILTKLYSSNVLFHSLF"
ORIGIN

Alignment Scores:
Pred. No.: 1.04e-80 Length: 487
Score: 821.00 Matches: 153
Percent Similarity: 97.53% Conservative: 5
Best Local Similarity: 94.44% Mismatches: 4
Query Match: 66.16% Indels: 0
DB: 10 Gaps: 0

US-09-914-053A-5 (1-235) x RNO517198 (1-487)

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Qy         40 LeuLysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIle 59
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 CTGAAGGCTGGAGAGGACCGGGCCATCCTGCTTGGACTGGCCATGATGGTGTGCTCCATC 61

Qy         60 MetMetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyrMetGlnSerValTrpThr 79
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 ATGATGTACTTCCTACTGGGAATCACACTGCTGCGCTCGTACATGCAGAGTGTGTGGACA 121

Qy         80 GluGluSerGlnCysThrLeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPhe 99
              ||||||:::|||||||  |||||||||  ||||||||||||||||||||||||||||||||
Db        122 GAAGAAGCCCAGTGTGCCCTGCTGAATGTGTCAATCACAGAAACATTTAACTGTTCCTTC 181

Qy        100 SerCysGlyProAspCysTrpLysLeuSerGlnTyrProCysLeuGlnValTyrValAsn 119
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        182 AGCTGTGGGCCTGACTGCTGGAAGCTCTCTCAGTACCCTTGCCTGCAGGTATACGTGAAC 241

Qy        120 LeuThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsn 139
              ||||||||||||||||||||||||||||||||||||||||||||||||:::|||||||||
Db        242 CTGACATCTTCTGGGGAGAAGCTCCTCCTCTACCACACAGAAGAGACCATGAAGATCAAT 301

Qy        140 GlnLysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuVal 159
              ||||||||||||||||||||||||||  ||||||||||||||||||||||||||||||||
Db        302 CAAAAGTGCTCCTATATTCCTAAGTGTGGAAACAACTTTGAGGAGTCCATGTCCCTTGTG 361

Qy        160 AsnValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGlu 179
              :::|||||||||||||||||||::::::||||||||  ||||||||||||||||||||
Db        362 AGTGTCGTCATGGAAAACTTCAGGAGACACCAACACTTCCCCTGCTATTCTGACCCAGAA 421

Qy        180 GlyAsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSer 199
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        422 GGGAACCAAAAGAGCGTCATCCTGACCAAACTCTATAGCTCCAATGTGCTGTTCCATTCT 481

Qy        200 LeuPhe 201
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Db        482 CTCTTC 487
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RESULT 14
AC117457
LOCUS AC117457 204899 bp DNA linear PRI 25-FEB-2003
DEFINITION Homo sapiens 3 BAC RP11-385J1 (Roswell Park Cancer Institute Human BAC Library) complete sequence.
ACCESSION AC117457
VERSION AC117457.11 GI:28557825
KEYWORDS HTG.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 204899)
AUTHORS Muzny,D.M., Adams,C., Adio-Oduola,B., Ali-osman,F.R., Allen,C., Alsbrooks,S.L., Amaratunge,H.C., Are,J.R., Ayele,M., Banks,T., Barbaria,J., Benton,J., Bimage,K., Blankenburg,K., Bonnin,D., Bouck,J., Bowie,S., Brieva,M., Brown,E., Brown,M., Bryant,N.P., Buhay,C., Burch,P., Burkett,C., Burrell,K.L., Byrd,N.C., Carron,T.F., Carter,M., Cavazos,S.R., Chacko,J., Chavez,D., Chen,G., Chen,R., Chen,Z., Chowdhry,I., Christopoulos,C., Cleveland,C.D., Cox,C., Coyle,M.D., Dathorne,S.R., David,R., Davila,M.L., Davis,C., Davy-Carroll,L., Dederich,D.A., Delaney,K.R., Delgado,O., Denn,A.L., Ding,Y., Dinh,H.H., Douthwaite,K.J., Draper,H., Dugan-Rocha,S., Durbin,K.J., Earnhart,C., Edgar,D., Edwards,C.C., Elhaj,C., Escotto,M., Falls,T., Ferraguto,D., Flagg,N., Ford,J., Foster,P., Frantz,P., Gabisi,A., Gao,J., Garcia,A., Garner,T., Garza,N., Gill,R., Gorrell,J.H., Guevara,W., Gunaratne,P., Hale,S., Hamilton,K., Harris,C., Harris,K., Hart,M., Havlak,P., Hawes,A., He,X., Hernandez,J., Hernandez,O., Hodgson,A., Hogues,M., Holloway,C.,

Hollins,B., Homsi,F., Howard,S., Huber,J., Hulyk,S., Hume,J., Jackson,L.E., Jacobson,B., Jia,Y., Johnson,R., Jolivet,S., Joudah,S., Karlsson,E., Kelly,S., Khan,U., King,L., Korvah,J., Kovar,C., Kratovic,J., Kureshi,A., Landry,N., Leal,B., Lewis,L.C., Lewis,L., Li,J., Li,Z., Lichtarge,O., Lieu,C., Liu,J., Liu,W., Loulseged,H., Lozado,R.J., Lu,X., Lucier,A., Lucier,R., Luna,R., Ma,J., Maheshwari,M., Mapua,P., Martin,R., Martindale,A., Martinez,E., Massey,E., Mawhiney,E., McLeod,M.P., Meador,M., Mei,G., Metzker,M., Miner,G., Miner,Z., Mitchell,T., Mohabbat,K., Moore,S., Morgan,M., Moorish,T., Morris,S., Moser,M., Neal,D., Nelson,D., Newtson,J., Newtson,N., Nguyen,A., Nguyen,N., Nguyen,N., Nickerson,E., Nwokenkwo,S., Oguh,M., Okwuonu,G., Oragunye,N., Oviedo,R., Pace,A., Payton,B., Peery,J., Perez,L., Peters,L., Pickens,R., Primus,E., Pu,L.L., Quiles,M., Ren,Y., Rives,M., Rojas,A., Rojubokan,I., Rolfe,M., Ruiz,S., Savery,G., Scherer,S., Scott,G., Shen,H., Shooshtari,N., Sisson,I., Sodergren,E., Sonaike,T., Sparks,A., Stanley,H., Stone,H., Sutton,A., Svatek,A., Tabor,P., Tamerisa,A., Tamerisa,K., Tang,H., Tansey,J., Taylor,C., Taylor,T., Telfrod,B., Thomas,N., Thomas,S., Usmani,K., Vasquez,L., Vera,V., Villalon,D., Vinson,R., Wang,Q., Wang,S., Ward-Moore,S., Warren,R., Washington,C., Watlington,S., Williams,G., Williamson,A., Wleczyk,R., Wooden,S., Worley,K., Wu,C., Wu,Y., Wu,Y.F., Zhou,J., Zorrilla,S., Naylor,S.L., Weinstock,G. and Gibbs,R.

TITLE Direct Submission
JOURNAL Unpublished
REFERENCE 2 (bases 1 to 204899)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (10-APR-2002) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 3 (bases 1 to 204899)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (22-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
REFERENCE 4 (bases 1 to 204899)
AUTHORS Worley,K.C.
TITLE Direct Submission
JOURNAL Submitted (25-FEB-2003) Human Genome Sequencing Center, Department of Molecular and Human Genetics, Baylor College of Medicine, One Baylor Plaza, Houston, TX 77030, USA
COMMENT On Feb 25, 2003 this sequence version replaced gi:28467084.
INFORMATION: http://www.hgsc.bcm.tmc.edu/ or email gc-help@bcm.tmc.edu

CLONE LENGTH: This sequence does not necessarily represent the entire insert of this clone. Overlapping regions of clones are only sequenced and submitted once, so the sequence for the remainder of the insert may be found in the record for the adjacent clones. Overlapping clones are noted at the beginning and end of the Features listing.

ANNOTATION OF FEATURES:
STSs are identified using ePCR (Genome Res. 7:541-550) searches of a local database that includes entries from dbSTS, GDB, and local mapping efforts.
Repeats are identified using RepeatMasker (A. Smit and P. Green, unpublished.) for Human and Mouse sequences.
Genes and Region of sequence similarity are identified by BLAST (Nuc. Acids Res. 25:3389-3402) similarity (expect < 1e-34) to the EST and cDNA sequences. Genes demonstrate at least two exons flanked by consensus splice sites that maintained sequence continuity across the splice junctions. Sequences that are not identical matches are annotated as similar.

SEQUENCING READ COVERAGE:Sequencing is completed to a minimum standard of double strand coverage with a minimum of 2 clones and 2 reads with no ambiguities or 2 chemistries with a minimum of 2 clones and 3 reads with no ambiguities. If the sequence quality for a region does not meet this standard, it will be indicated in the annotation as Low Coverage.

QUALITY OF INDIVIDUAL BASES:This sequence meets stringent quality standards - estimated error rate less than 1 per 10,000 bases. Reports of lowest quality individual bases and measures of base quality are listed below. Description of the metrics can be found at URL:
http://www.hgsc.bcm.tmc.edu:8088/quality.info/genbank.annotation.html.

FEATURES Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:9606"
/chromosome="3"
/clone="RP11-385J1"
misc_feature complement(1. .2000)
/note="overlaps bases 1. .2000 of clone AC139661"
/function="clone overlap"
repeat_region complement(501. .659)
/rpt_family="L2"
repeat_region complement(1481. .1546)
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repeat_region 1611. .1689
/rpt_family="MLT1B"
repeat_region 1694. .1879
/rpt_family="MER2"
repeat_region 1893. .1922
/rpt_family="AT_rich"
repeat_region 1964. .2082
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repeat_region 2083. .2421
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repeat_region 2422. .2587
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repeat_region complement(2948. .3005)
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repeat_region complement(5059. .5175)
/rpt_family="MER20"
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/rpt_family="MIR"
repeat_region complement(5578. .5707)
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repeat_region complement(7006. .7250)
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repeat_region 7575. .9962
/rpt_family="L2"
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repeat_region complement(12469. .13201)
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repeat_region 13643. .13814
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repeat_region 13815. .13840
/rpt_family="(TTG)n"
repeat_region 13841. .13878
/rpt_family="L2"
repeat_region complement(13891. .13953)
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repeat_region complement(14053. .14222)
/rpt_family="FRAM"
repeat_region 15888. .15985
/rpt_family="MER5B"
repeat_region 15990. .16149
/rpt_family="MIR"
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/rpt_family="L2"

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     repeat_region   19374. .19673
                     /rpt_family="AluSp"
     repeat_region   19674. .19760
                     /rpt_family="L1MA8"
     repeat_region   20088. .20127
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     repeat_region   20874. .20893
                     /rpt_family="(GA)n"
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Alignment Scores:
Pred. No.:              2.54e-43        Length:         204899
Score:                  510.50          Matches:        120
Percent Similarity:     52.00%          Conservative:   23
Best Local Similarity:  43.64%          Mismatches:     31
Query Match:            41.14%          Indels:         103
DB:                     9               Gaps:           6

US-09-914-053A-5 (1-235) x AC117457 (1-204899)

Qy         44 GluAspArgAlaIleLeuLeuGlyLeuAlaMetMetValCysSerIleMetMetTyrPhe 63
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Db     176994 AAAGATAAGAGTATACTACTTTCCCTGAGAGAACTGGTAAGTTTTTATGTTATGTGGAC- 177052

Qy         64 LeuLeuGlyIleThr---------------------------------------------- 68
                  |||   |||
Db     177053 AGATGTGGACAGACAAAATGATGGCAGAGTTGACATTCTGATTCCATAAAGAAGTATGTT 177112

Qy         69 ---------LeuLeuArgSerTyrMetGlnSerValTrpThrGluGluSerGlnCysThr 85
                     :::::::::::|||         :::|||   :::||||||
Db     177113 CAATAGAAAATAATTAAAACCTACCATACCTAGCTATGGCAAAAAGAATCC--------- 177163

Qy         86 LeuLeuAsnAlaSerIleThrGluThrPheAsnCysSerPheSerCysGlyProAsp--- 104
                               |||:::||||||      ::::::|||      :::
Db     177164 -----------------TGGGAATCATTTAATTTATTTTACGCATGCAACATGGAATGA 177205

Qy        104 ------------------------------------------------------------ 104

Db     177206 TTAAATCAAGCTAATTAACATATCTATCATTTTATTTCAATCAATAAATAATATATGGGT 177265

Qy        105 ------------------------------------------------------Cys--- 105
                                                                      |||
Db     177266 GAGCAATCAAGGGACATCTTGGTCAGATACCTTAAAACATTGTTTTAATCAATGTGTTAT 177325

Qy        106 ------------------------------------------------------TrpLysLeu 108
                                                                      |||   :::
Db     177326 TTATTAGGGTTTCCAAAGGCACCAGTTTGAATATGAAAAGAATAACCACCATGGTT-ATT 177384

Qy        109 SerGln-----------------------TyrProCysLeuGlnValTyrValAsnLeu 120
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Db     177385 TCACAGATCACTAATTTGGACACAATACTCCACCCCCTCCTAGAGTCTCAAACACACATA 177444

Qy        121 ThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGluGluThrIleLysIleAsnGln 140
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Db     177445 GTATCTTCTAGTAACAGTTTA-------------------------TCTTATTCTCCA 177477

Qy        141 LysCysSerTyrIleProLysCysGlyLysAsnPheGluGluSerMetSerLeuValAsn 160
              :::||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     177478 CAGTGCTCCTATATACCTAAATGTGGAAAAAATTTTGAAGAATCCATGTCCCTGGTGAAT 177537

Qy        161 ValValMetGluAsnPheArgLysTyrGlnHisPheSerCysTyrSerAspProGluGly 180
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Db     177538 GTTGTCATGGAAAACTTCAGGAAGTATCAACACTTCTCCTGCTATTCTGACCCAGAAGGA 177597

Qy        181 AsnGlnLysSerValIleLeuThrLysLeuTyrSerSerAsnValLeuPheHisSerLeu 200
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Db     177598 AACCAGAAGAGTGTTATCCTAACAAAACTCTACAGTTCCAACGTGCTGTTCCATTCACTC 177657

Qy        201 PheTrpProThrCysMetMetAlaGlyGlyValAlaIleValAlaMetValLysLeuThr 220
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Db     177658 TTCTGGCCAACCTGTATGATGGCTGGGGGTGTGGCAATTGTTGCCATGGTGAAACTTACA 177717

Qy        221 GlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIleAsnArg 235
              |||||||||||||||||||||||||||||||||||||||||||||
Db     177718 CAGTACCTCTCCCTACTATGTGAGAGGATCCAACGGATCAATAGA 177762

RESULT 15
CCU67865
LOCUS       CCU67865                815 bp    mRNA    linear   VRT 21-JUL-1998
DEFINITION  Coturnix coturnix putative potassium channel regulatory subunit
            (CO6) mRNA, complete cds.
ACCESSION   U67865
VERSION     U67865.1  GI:1527200
KEYWORDS    .
SOURCE      Coturnix coturnix (common quail)
  ORGANISM  Coturnix coturnix
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
            Phasianinae; Coturnix.
REFERENCE   1  (bases 1 to 815)
  AUTHORS   Oberst,C., Weiskirchen,R., Hartl,M. and Bister,K.
  TITLE     Suppression in transformed avian fibroblasts of a gene (CO6)
            encoding a membrane protein related to mammalian potassium channel
            regulatory subunits
  JOURNAL   Oncogene 14 (9), 1109-1116 (1997)
  MEDLINE   97224079
   PUBMED   9070660
REFERENCE   2  (bases 1 to 815)
  AUTHORS   Oberst,C. and Bister,K.
  TITLE     Direct Submission
  JOURNAL   Submitted (23-AUG-1996) Institute of Biochemistry, University of
            Innsbruck, Peter-Mayr-Strasse 1a, Innsbruck A-6020, Austria
FEATURES             Location/Qualifiers
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                     /db_xref="taxon:9091"
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                     /dev_stage="embryo"
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                     /gene="CO6"
     CDS             153. .755
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                     potassium channel regulatory subunits homolog"
                     /codon_start=1
                     /product="putative potassium channel regulatory subunit"
                     /protein_id="AAC26967.1"
                     /db_xref="GI:1527201"
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                     KSVWTTETICKVLKANIKDKTHCTNSEGSEDEDIFHYPCLQVWVNLTASGQEVMLYHT
                     EDTLERNPKCSYVPGNSENSKEVKARIETIASNFKKYQTFPCYYDPGGMQTNVILSRL
                     YPPKGLLFTFLWPTLMFTGGCLIIVLVKISQYFSVLSARQ"
ORIGIN

Alignment Scores:
Pred. No.:              3.55e-46        Length:         815
Score:                  509.00          Matches:        94
Percent Similarity:     67.66%          Conservative:   42
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Best Local Similarity: 46.77% Mismatches: 65
Query Match: 41.02% Indels: 0
DB: 5 Gaps: 0

US-09-914-053A-5 (1-235) x CCU67865 (1-815)

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Qy          34 ArgLysThrValThrAlaLeuLysAlaGlyGluAspArgAlaIleLeuLeuGlyLeuAla 53
               :::|||  |||||||||  |||  ||||||  |||||||:::  |||||||||
Db         162 AAAAAGCTGGTGACTGCGCAGAAGAGAGGAGAGACAAGGGCCCTGTGTCTGGGACTGGGG 221

Qy          54 MetMetValCysSerIleMetMetTyrPheLeuLeuGlyIleThrLeuLeuArgSerTyr 73
               |||:::  ||||||:::|||||||||||||  :::|||||||||:::::::     |||
Db         222 ATGGTCGCATGCTCCATGATGATGTACTTCTTTATTGGGATTACAATTGTGCCATTCTAC 281

Qy          74 MetGlnSerValTrpThrGluGluSerGlnCysThrLeuLeuAsnAlaSerIleThrGlu 93
                  :::||||||||||||  |||:::  |||  :::|||  |||:::|||  :::
Db         282 ACTAAAAGTGTCTGGACAACAGAAACTATATGCAAGGTCCTCAAAGCCAACATCAAGGAC 341

Qy          94 ThrPheAsnCysSerPheSerCysGlyProAspCysTrpLysLeuSerGlnTyrProCys 113
                  :::|||:::  |||  |||  :::        :::      |||||||||
Db         342 AAAACCCACTGCACAAACAGCGAAGGCTCAGAGGATGAAGATATTTTTCATTACCCTTGC 401

Qy         114 LeuGlnValTyrValAsnLeuThrSerSerGlyGluLysLeuLeuLeuTyrHisThrGlu 133
               |||||||||:::|||||||||||:::||||||:::::::::::::|||||||||||||
Db         402 CTACAGGTGTGGGTTAATCTGACAGCCTCAGGACAAGAGGTCATGTTGTATCACACTGAA 461

Qy         134 GluThrIleLysIleAsnGlnLysCysSerTyrIleProLysCysGlyLysAsnPheGlu 153
               :::|||::::::  |||  ||||||||||:::|||        :::|||  :::
Db         462 GATACCCTGGAAAGAAATCCAAAGTGCTCATATGTCCCTGGCAACTCAGAGAACTCCAAA 521

Qy         154 GluSerMetSerLeuValAsnValValMetGluAsnPheArgLysTyrGlnHisPheSer 173
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Db         522 GAAGTGAAAGCACGAATAGAAACAATTGCAAGCAATTTTAAAAAATATCAGACTTTCCCA 581

Qy         174 CysTyrSerAspProGluGlyAsnGlnLysSerValIleLeuThrLysLeuTyrSerSer 193
               ||||||  ||||||  |||  |||  :::|||||||||:::::||||||
Db         582 TGCTACTACGACCCAGGAGGAATGCAGACCAACGTCATTTTAAGCAGACTTTATCCCCCC 641

Qy         194 AsnValLeuPheHisSerLeuPheTrpProThrCysMetMetAlaGlyGlyValAlaIle 213
                  |||      :::      |||||||||  |||      ||||||     |||
Db         642 AAAGGCCTCCTTTTCACTTTCCTTTGGCCCACACTCATGTTTACCGGTGGATGTCTGATT 701

Qy         214 ValAlaMetValLysLeuThrGlnTyrLeuSerLeuLeuCysGluArgIleGlnArgIle 233
               :::   :::||||||:::::::||||||   |||:::|||      |||        :::
Db         702 ATCGTCCTGGTAAAAATCAGCCAGTATTTTTCTGTTCTTTCTGCTCGGCAGTAGGAAGTA 761

Qy         234 Asn 234
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Search completed: November 7, 2004, 02:31:33
Job time : 3167 secs